BEST AVAILABLE IMAGES

Defective images within this document are accurate representation of The original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

As rescanning documents *will not* correct images, please do not report the images to the Image Problem Mailbox.

Figure 1

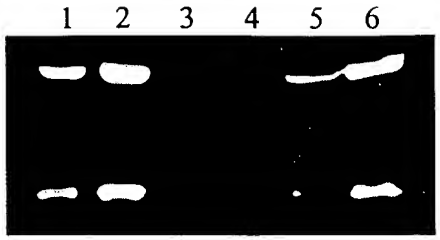

Figure 2

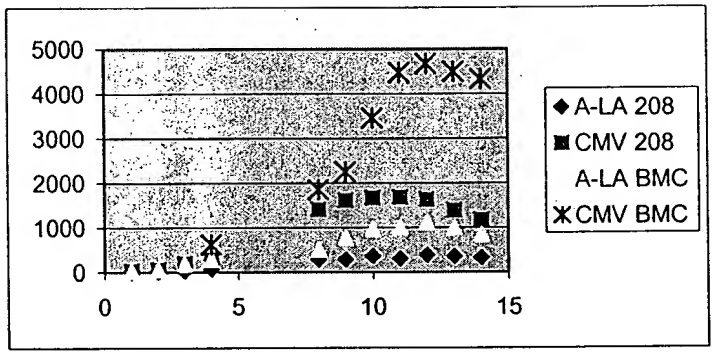

Figure 3

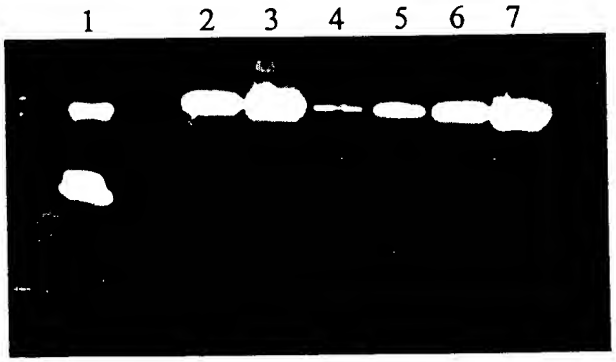

Figure 4
SEQ ID NO:1
Hybrid Human-Bovine Alpha-Lactalbumin Promoter

```
1     GATCAGTCCTGGGTGGTCATTGAAAGGACTGATGCTGAAGTTGAAGCTCC
51    AATACTTTGGCCACCTGATGCGAAGAACTGACTCATGTGATAAGACCCTG
101   ATACTGGGAAAGATTGAAGGCAGGAGGAGAAGGGATGACAGAGGATGGAA
151   GAGTTGGATGGAATCACCAACTCGATGGACATGAGTTTGAGCAAGCTTCC
201   AGGAGTTGGTAATGGGCAGGGAAGCCTGGCGTGCTGCAGTCCATGGGGTT
251   GCAAAGAGTTGGACACTACTGAGTGACTGAACTGAACTGATAGTGTAATC
301   CATGGTACAGAATATAGGATAAAAAAGAGGAAGAGTTTGCCCTGATTCTG
351   AAGAGTTGTAGGATATAAAAGTTTAGAATACCTTTAGTTTGGAAGTCTTA
401   AATTATTTACTTAGGATGGGTACCCACTGCAATATAAGAAATCAGGCTTT
451   AGAGACTGATGTAGAGAGAATGAGCCCTGGCATACCAGAAGCTAACAGCT
501   ATTGGTTATAGCTGTTATAACCAATATATAACCAATATATTGGTTATATA
551   GCATGAAGCTTGATGCCAGCAATTTGAAGGAACCATTTAGAACTAGTATC
601   CTAAACTCTACATGTTCCAGGACACTGATCTTAAAGCTCAGGTTCAGAAT
651   CTTGTTTTATAGGCTCTAGGTGTATATTGTGGGGCTTCCCTGGTGGCTCA
701   GATGGTAAAGTGTCTGCCTGCAATGTGGGTGATCTGGGTTCGATCCCTGG
751   CTTGGGAAGATCCCCTGGAGAAGGAAATGGCAACCCACTCTAGTACTCTT
801   ACCTGGAAAATTCCATGGACAGAGGAGCCTTGTAAGCTACAGTCCATGGG
851   ATTGCAAAGAGTTGAACACAACTGAGCAACTAAGCACAGCACAGTACAGT
900   ATACACCTGTGAGGTGAAGTGAAGTGAAGGTTCAATGCAGGGTCTCCTGC
951   ATTGCAGAAAGATTCTTTACCATCTGAGCCACCAGGGAAGCCCAAGAATA
1001  CTGGAGTGGGTAGCCTATTCCTTCTCCAGGGGATCTTCCCATCCCAGGAA
1051  TTGAACTGGAGTCTCCTGCATTTCAGGTGGATTCTTCACCAGCTGAACTA
1101  CCAGGTGGATACTACTCCAATATTAAAGTGCTTAAAGTCCAGTTTTCCCA
1151  CCTTTCCCAAAAAGGTTGGGTCACTCTTTTTTAACCTTCTGTGGCCTACT
1201  CTGAGGCTGTCTACAAGCTTATATATTTATGAACACATTTATTGCAAGTT
1251  GTTAGTTTTAGATTTACAATGTGGTATCTGGCTATTTAGTGGTATTGGTG
1301  GTTGGGGATGGGGAGGCTGATAGCATCTCAGAGGGCAGCTAGATACTGTC
1351  ATACACACTTTTCAAGTTCTCCATTTTTGTGAAATAGAAAGTCTCTGGAT
1401  CTAAGTTATATGTGATTCTCAGTCTCTGTGGTCATATTCTATTCTACTCC
1451  TGACCACTCAACAAGGAACCAAGATATCAAGGGACACTTGTTTTGTTTCA
1501  TGCCTGGGTTGAGTGGGCCATGACATATGTTCTGGGCCTTGTTACATGGC
1551  TGGATTGGTTGGACAAGTGCCAGCTCTGATCCTGGGACTGTGGCATGTGA
1601  TGACATACACCCCCTCTCCACATTCTGCATGTCTCTAGGGGGGAAGGGGG
1651  AAGCTCGGTATAGAACCTTTATTGTATTTTCTGATTGCCTCACTTCTTAT
1701  ATTGCCCCCATGCCCTTCTTTGTTCCTCAAGTAACCAGAGACAGTGCTTC
1751  CCAGAACCAACCCTACAAGAAACAAAGGGCTAAACAAAGCCAAATGGGAA
1801  GCAGGATCATGGTTTGAACTCTTTCTGGCCAGAGAACAATACCTGCTATG
1851  GACTAGATACTGGGAGAGGGAAAGGAAAAGTAGGGTGAATTATGGAAGGA
1901  AGCTGGCAGGCTCAGCGTTTCTGTCTTGGCATGACCAGTCTCTCTTCATT
1951  CTCTTCCTAGATGTAGGGCTTGGTACCAGAGCCCCTGAGGCTTTCTGCAT
2001  GAATATAAATATATGAAACTGAGTGATGCTTCCATTTCAGGTTCTTGGGG
2051  GCGCCGAATTCGAGCTCGGTACCCGGGGATCTCGAGGGGGGGCCCGGTAC
2101  C
```

1 - 1525	Bovine alpha lactalbumin 5' flanking region (-2000 to -550 from the bovine alpha-lactalbumin transcription start point)
1526 - 2056	Human alpha-lactalbumin 5' flanking region (-600 to +15 from the human alpha-lactalbumin transcription start point)
2057 - 2101	Multiple cloning site

Figure 5
SEQ ID NO:2
Mutated PPE Sequence

```
1      GATTACTTACTGGCAGGTGCTGGGGGCTTCCGAGACAATCGCGAACATCT
51     ACACCACACAACACCGCCTCGACCAGGGTGAGATATCGGCCGGGGACGCG
101    GCGGTGGTAATTACAAGCGAGGATCCGATTACTTACTGGCAGGTGCTGGG
151    GGCTTCCGAGACAATCGCGAACATCTACACCACACAACACCGCCTCGACC
201    AGGGTGAGATATCGGCCGGGGACGCGGCGGTGGTAATTACAAGCG
```

1 - 119	Mutated PPE
120 -126	Linker
127 - 245	Mutated PPE

Figure 6
SEQ ID NO:3
IRES-Signal Peptide Sequence

```
1      GGAATTCGCCCCTCTCCCTCCCCCCCCCCTAACGTTACTGGCCGAAGCCG
51     CTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTTCCACCATAT
101    TGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGTCTTCTTG
151    ACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGAATGCAAGGTCT
201    GTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAA
251    CAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGAC
301    AGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGC
351    GGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCA
401    AATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCAGAAG
451    GTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCTTTAC
501    ATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCCCCGAACCACGGGG
551    ACGTGGTTTTCCTTTGAAAAACACGATGATAATATGGCCTCCTTTGTCTC
601    TCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCCGGCGCCATGG
651    GATATCTAGATCTCGAGCTCGCGAAAGCTT
```

1 - 583	IRES
584 - 640	Modified bovine alpha-lactalbumin signal peptide coding region
641 - 680	Multiple cloning site

Figure 7a
SEQ ID NO:4
CMV MN14 Vector

1 CGGATCCGGCCATTAGCCATATTATTCATTGGTTATATAGCATAAATCAA
51 TATTGGCTATTGGCCATTGCATACGTTGTATCCATATCATAATATGTACA
101 TTTATATTGGCTCATGTCCAACATTACCGCCATGTTGACATTGATTATTG
151 ACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATA
201 TATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGAC
251 CGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATA
301 GTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACG
351 GTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGC
401 CCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAG
451 TACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGT
501 CATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTG
551 GATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTC
601 AATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCG
651 TAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCATGTACGGTGGG
701 AGGTCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGCCTGGAGA
751 CGCCATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCAG
801 CCTCCGCGGCCCCAAGCTTCTCGACGGATCCCCGGGAATTCAGGACCTCA
851 CCATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGT
901 GTCCACTCCGAGGTCCAACTGGTGGAGAGCGGTGGAGGTGTTGTGCAACC
951 TGGCCGGTCCCTGCGCCTGTCCTGCTCCGCATCTGGCTTCGATTTCACCA
1001 CATATTGGATGAGTTGGGTGAGACAGGCACCTGGAAAAGGTCTTGAGTGG
1051 ATTGGAGAAATTCATCCAGATAGCAGTACGATTAACTATGCGCCGTCTCT
1101 AAAGGATAGATTTACAATATCGCGAGACAACGCCAAGAACACATTGTTCC
1151 TGCAAATGGACAGCCTGAGACCCGAAGACACCGGGGTCTATTTTTGTGCA
1201 AGCCTTTACTTCGGCTTCCCCTGGTTTGCTTATTGGGGCCAAGGGACCCC
1251 GGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGG
1301 CACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTG
1351 GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
1401 CCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGAC
1451 TCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
1501 CAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGA
1551 CAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGT
1601 GCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCA
1651 AAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGT
1701 GGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACG
1751 TGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG
1801 TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGA
1851 CTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCC
1901 CAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAA
1951 CCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCA
2001 GGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCG
2051 TGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT
2101 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGT
2151 GGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGC
2201 ACGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCC
2251 GGGAAATGAAAGCCGAATTCGCCCCTCTCCCTCCCCCCCCCCTAACGTTA
2301 CTGGCCGAAGCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTA
2351 TTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGG
2401 CCCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAG
2451 GAATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCT
2501 TCTTGAAGACAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCC
2551 CCCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATA
2601 CACCTGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTT
2651 GTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAA
2701 GGATGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGT
2751 GCACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCC
2801 CCGAACCACGGGGACGTGGTTTTCCTTTGAAAAACACGATGATAATATGG

Figure 7b

```
2851   CCTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAG
2901   GCCGACATCCAGCTGACCCAGAGCCCAAGCAGCCTGAGCGCCAGCGTGGG
2951   TGACAGAGTGACCATCACCTGTAAGGCCAGTCAGGATGTGGGTACTTCTG
3001   TAGCCTGGTACCAGCAGAAGCCAGGTAAGGCTCCAAAGCTGCTGATCTAC
3051   TGGACATCCACCCGGCACACTGGTGTGCCAAGCAGATTCAGCGGTAGCGG
3101   TAGCGGTACCGACTTCACCTTCACCATCAGCAGCCTCCAGCCAGAGGACA
3151   TCGCCACCTACTACTGCCAGCAATATAGCCTCTATCGGTCGTTCGGCCAA
3201   GGGACCAAGGTGGAAATCAAACGAACTGTGGCTGCACCATCTGTCTTCAT
3251   CTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT
3301   GCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTG
3351   GATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA
3401   CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAG
3451   CAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGC
3501   CTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGATC
3551   TAGGCCTCCTAGGTCGACATCGATAAAATAAAAGATTTTATTTAGTCTCC
3601   AGAAAAAGGGGGGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCTAGCT
3651   TAAGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGA
3701   GAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGGCCAA
3751   ACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACA
3801   GATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTC
3851   CTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCC
3901   CTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGAC
3951   CTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCG
4001   CTTCTGTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAAC
4051   CCCTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCCGGGTACCC
4101   GTGTATCCAATAAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTG
4151   TTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTC
4201   TTTCATT
```

1 - 812	CMV promoter/enhancer
853-855	MN14 antibody heavy chain gene signal peptide start codon
2257 - 2259	MN14 antibody heavy chain gene start codon
2271 - 2846	EMCV IRES
2847 - 2849	Bovine alpha-lactalbumin signal peptide start codon
2904 - 2906	First codon mature MN14 antibody light chain gene
3543 - 3544	MN14 antibody light chain gene stop codon
3614 - 4207	MoMuLV 3' LTR

Figure 8a
SEQ ID NO:5
CMV LL2 Vector

```
1     GGATCCGGCCATTAGCCATATTATTCATTGGTTATATAGCATAAATCAAT
51    ATTGGCTATTGGCCATTGCATACGTTGTATCCATATCATAATATGTACAT
101   TTATATTGGCTCATGTCCAACATTACCGCCATGTTGACATTGATTATTGA
151   CTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATAT
201   ATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACC
251   GCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAG
301   TAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGG
351   TAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCC
401   CCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGT
451   ACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTC
501   ATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGG
551   ATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCA
601   ATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGT
651   AACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCATGTACGGTGGGA
701   GGTCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGCCTGGAGAC
751   GCCATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCAGC
801   CTCCGCGGCCCCAAGCTTCTCGACGGATCCCCGGGAATTCAGGACCTCAC
851   CATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTG
901   TCCACTCCCAGGTCCAGCTGGTCCAATCAGGGGCTGAAGTCAAGAAACCT
951   GGGTCATCAGTGAAGGTCTCCTGCAAGGCTTCTGGCTACACCTTTACTAG
1001  CTACTGGCTGCACTGGGTCAGGCAGGCACCTGGACAGGGTCTGGAATGGA
1051  TTGGATACATTAATCCTAGGAATGATTATACTGAGTACAATCAGAACTTC
1101  AAGGACAAGGCCACAATAACTGCAGACGAATCCACCAATACAGCCTACAT
1151  GGAGCTGAGCAGCCTGAGGTCTGAGGACACGGCATTTTATTTTTGTGCAA
1201  GAAGGGATATTACTACGTTCTACTGGGGCCAAGGCACCACGGTCACCGTC
1251  TCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTC
1301  CAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACT
1351  ACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCCCTGACCAGC
1401  GGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCT
1451  CAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACA
1501  TCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAGAGTT
1551  GAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTGCCCAGCACC
1601  TGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGG
1651  ACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGAC
1701  GTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGT
1751  GGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCA
1801  CGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAAT
1851  GGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCAT
1901  CGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGT
1951  ACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAGGTCAGCCTG
2001  ACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGA
2051  GAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGG
2101  ACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTGGACAAGAGC
2151  AGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCACGAGGCTCT
2201  GCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCCGGGAAATGAA
2251  AGCCGAATTCGCCCCTCTCCCTCCCCCCCCCCTAACGTTACTGGCCGAAG
2301  CCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTTCCACCA
2351  TATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGTCTTC
2401  TTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGAATGCAAGG
2451  TCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGAC
2501  AAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGC
2551  GACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAA
2601  GGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAG
2651  TCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCAG
2701  AAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCTT
2751  TACATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCCCCGAACCACG
2801  GGGACGTGGTTTTCCTTTGAAAAACACGATGATAATATGGCCTCCTTTGT
```

Figure 8b

```
2851  CTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCCGACATCC
2901  AGCTGACCCAGTCTCCATCATCTCTGAGCGCATCTGTTGGAGATAGGGTC
2951  ACTATGAGCTGTAAGTCCAGTCAAAGTGTTTTATACAGTGCAAATCACAA
3001  GAACTACTTGGCCTGGTACCAGCAGAAACCAGGGAAAGCACCTAAACTGC
3051  TGATCTACTGGGCATCCACTAGGGAATCTGGTGTCCCTTCGCGATTCTCT
3101  GGCAGCGGATCTGGGACAGATTTTACTTTCACCATCAGCTCTCTTCAACC
3151  AGAAGACATTGCAACATATTATTGTCACCAATACCTCTCCTCGTGGACGT
3201  TCGGTGGAGGGACCAAGGTGCAGATCAAACGAACTGTGGCTGCACCATCT
3251  GTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTC
3301  TGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGT
3351  GGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACA
3401  GAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCT
3451  GAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCC
3501  ATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT
3551  TAGAGATCTAGGCCTCCTAGGTCGACATCGATAAAATAAAAGATTTTATT
3601  TAGTCTCCAGAAAAAGGGGGGAATGAAAGACCCCACCTGTAGGTTTGGCA
3651  AGCTAGCTTAAGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTG
3701  AGAATAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATA
3751  TGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGC
3801  CAAGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTA
3851  AGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCG
3901  GTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCC
3951  CCAAGGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTC
4001  GCTTCTCGCTTCTGTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAG
4051  CCCACAACCCCTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCC
4101  GGGTACCCGTGTATCCAATAAACCCTCTTGCAGTTGCATCCGACTTGTGG
4151  TCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAG
4201  GTCTTTCATT
```

1 - 812	CMV promoter/enhancer
852 - 854	LL2 antibody heavy chain signal peptide start codon
2247 - 2249	LL2 antibody heavy chain stop codon
2261 - 2836	EMCV IRES
2837 - 2839	Bovine alpha-lactalbumin signal peptide start codon
2894-2896	First codon of mature LL2 antibody light chain gene
3551 - 3553	LL2 antibody light chain gene stop codon
3622 - 4210	MoMuLV 3' LTR

Figure 9a
SEQ ID NO:6
MMTV MN14 Vector

```
1     CGAGCTTGGCAGAAATGGTTGAACTCCCGAGAGTGTCCTACACCTAGGGG
51    AGAAGCAGCCAAGGGGTTGTTTCCCACCAAGGACGACCCGTCTGCGCACA
101   AACGGATGAGCCCATCAGACAAAGACATATTCATTCTCTGCTGCAAACTT
151   GGCATAGCTCTGCTTTGCCTGGGGCTATTGGGGGAAGTTGCGGTTCGTGC
201   TCGCAGGGCTCTCACCCTTGACTCTTTCAATAATAACTCTTCTGTGCAAG
251   ATTACAATCTAAACAATTCGGAGAACTCGACCTTCCTCCTGAGGCAAGGA
301   CCACAGCCAACTTCCTCTTACAAGCCGCATCGATTTTGTCCTTCAGAAAT
351   AGAAATAAGAATGCTTGCTAAAAATTATATTTTTACCAATAAGACCAATC
401   CAATAGGTAGATTATTAGTTACTATGTTAAGAAATGAATCATTATCTTTT
451   AGTACTATTTTTACTCAAATTCAGAAGTTAGAAATGGGAATAGAAAATAG
501   AAAGAGACGCTCAACCTCAATTGAAGAACAGGTGCAAGGACTATTGACCA
551   CAGGCCTAGAAGTAAAAAAGGGAAAAAAGAGTGTTTTTGTCAAAATAGGA
601   GACAGGTGGTGGCAACCAGGGACTTATAGGGGACCTTACATCTACAGACC
651   AACAGATGCCCCCTTACCATATACAGGAAGATATGACTTAAATTGGGATA
701   GGTGGGTTACAGTCAATGGCTATAAAGTGTTATATAGATCCCTCCCCTTT
751   CGTGAAAGACTCGCCAGAGCTAGACCTCCTTGGTGTATGTTGTCTCAAGA
801   AAAGAAAGACGACATGAAACAACAGGTACATGATTATATTTATCTAGGAA
851   CAGGAATGCACTTTTGGGGAAAGATTTTCCATACCAAGGAGGGGACAGTG
901   GCTGGACTAATAGAACATTATTCTGCAAAAACTTATGGCATGAGTTATTA
951   TGATTAGCCTTGATTTGCCCAACCTTGCGGTTCCCAAGGCTTAAGTAAGT
1001  TTTTGGTTACAAACTGTTCTTAAAACAAGGATGTGAGACAAGTGGTTTCC
1051  TGACTTGGTTTGGTATCAAAGGTTCTGATCTGAGCTCTGAGTGTTCTATT
1101  TTCCTATGTTCTTTTGGAATTTATCCAAATCTTATGTAAATGCTTATGTA
1151  AACCAAGATATAAAAGAGTGCTGATTTTTTGAGTAAACTTGCAACAGTCC
1201  TAACATTCACCTCTTGTGTGTTTGTGTCTGTTCGCCATCCCGTCTCCGCT
1251  CGTCACTTATCCTTCACTTTCCAGAGGGTCCCCCCGCAGACCCCGGCGAC
1301  CCTCAGGTCGGCCGACTGCGGCAGCTGGCGCCCGAACAGGGACCCTCGGA
1351  TAAGTGACCCTTGTCTTTATTTCTACTATTTTGTGTTCGTCTTGTTTTGT
1401  CTCTATCTTGTCTGGCTATCATCACAAGAGCGGAACGGACTCACCTCAGG
1451  GAACCAAGCTAGCCCGGGGTCGACGGATCCGATTACTTACTGGCAGGTGC
1501  TGGGGGCTTCCGAGACAATCGCGAACATCTACACCACACAACACCGCCTC
1551  GACCAGGGTGAGATATCGGCCGGGGACGCGGCGGTGGTAATTACAAGCGA
1601  GATCCGATTACTTACTGGCAGGTGCTGGGGGCTTCCGAGACAATCGCGAA
1651  CATCTACACCACACAACACCGCCTCGACCAGGGTGAGATATCGGCCGGGG
1701  ACGCGGCGGTGGTAATTACAAGCGAGATCCCCGGGAATTCAGGACCTCAC
1751  CATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGTG
1801  TCCACTCCGAGGTCCAACTGGTGGAGAGCGGTGGAGGTGTTGTGCAACCT
1851  GGCCGGTCCCTGCGCCTGTCCTGCTCCGCATCTGGCTTCGATTTCACCAC
1901  ATATTGGATGAGTTGGGTGAGACAGGCACCTGGAAAAGGTCTTGAGTGGA
1951  TTGGAGAAATTCATCCAGATAGCAGTACGATTAACTATGCGCCGTCTCTA
2001  AAGGATAGATTTACAATATCGCGAGACAACGCCAAGAACACATTGTTCCT
2051  GCAAATGGACAGCCTGAGACCCGAAGACACCGGGGTCTATTTTTGTGCAA
2101  GCCTTTACTTCGGCTTCCCCTGGTTTGCTTATTGGGGCCAAGGGACCCCG
2151  GTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGC
2201  ACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGG
2251  TCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGCC
2301  CTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACT
2351  CTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCC
2401  AGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGAC
2451  AAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGTG
2501  CCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAA
2551  AACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGTG
2601  GTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGT
2651  GGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGT
2701  ACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGAC
2751  TGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCC
2801  AGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAAC
```

Figure 9b

```
2851  CACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCAG
2901  GTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGT
2951  GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTC
3001  CCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGTG
3051  GACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCA
3101  CGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCCG
3151  GGAAATGAAAGCCGAATTCGCCCCTCTCCCTCCCCCCCCCCTAACGTTAC
3201  TGGCCGAAGCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTAT
3251  TTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGC
3301  CCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGG
3351  AATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTT
3401  CTTGAAGACAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCC
3451  CCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATAC
3501  ACCTGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTTG
3551  TGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAG
3601  GATGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTG
3651  CACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCCC
3701  CGAACCACGGGGACGTGGTTTTCCTTTGAAAAACACGATGATAATATGGC
3751  CTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGG
3801  CCGACATCCAGCTGACCCAGAGCCCAAGCAGCCTGAGCGCCAGCGTGGGT
3851  GACAGAGTGACCATCACCTGTAAGGCCAGTCAGGATGTGGGTACTTCTGT
3901  AGCCTGGTACCAGCAGAAGCCAGGTAAGGCTCCAAAGCTGCTGATCTACT
3951  GGACATCCACCCGGCACACTGGTGTGCCAAGCAGATTCAGCGGTAGCGGT
4001  AGCGGTACCGACTTCACCTTCACCATCAGCAGCCTCCAGCCAGAGGACAT
4051  CGCCACCTACTACTGCCAGCAATATAGCCTCTATCGGTCGTTCGGCCAAG
4101  GGACCAAGGTGGAAATCAAACGAACTGTGGCTGCACCATCTGTCTTCATC
4151  TTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGTG
4201  CCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGG
4251  ATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGAC
4301  AGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGC
4351  AGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCC
4401  TGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGATCC
4451  CCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATAATCAACCTCTGGA
4501  TTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTT
4551  TTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCT
4601  TCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTGCTGTC
4651  TCTTTATGAGGAGTTGTGGCCCGTTGTCAGGCAACGTGGCGTGGTGTGCA
4701  CTGTGTTTGCTGACGCAACCCCCACTGGTTGGGGCATTGCCACCACCTGT
4751  CAGCTCCTTTCCGGGACTTTCGCTTTCCCCCTCCCTATTGCCACGGCGGA
4801  ACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGG
4851  GCACTGACAATTCCGTGGTGTTGTCGGGGAAATCATCGTCCTTTCCTTGG
4901  CTGCTCGCCTGTGTTGCCACCTGGATTCTGCGCGGGACGTCCTTCTGCTA
4951  CGTCCCTTCGGCCCTCAATCCAGCGGACCTTCCTTCCCGCGGCCTGCTGC
5001  CGGCTCTGCGGCCTCTTCCGCGTCTTCGCCTTCGCCCTCAGACGAGTCGG
5051  ATCTCCCTTTGGGCCGCCTCCCCGCCTGATCGATACCGTCAACATCGATA
5101  AAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAATGAAAGACCC
5151  CACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCAT
5201  GGAAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGGTCAGGAACA
5251  GATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTC
5301  CTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAA
5351  ACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACA
5401  GATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCA
5451  GATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTG
5501  AACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTCTGCTCCC
5551  CGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGCCAGTCCTCC
5601  GATTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACCCTCTTGCAG
5651  TTGCATCCGACTTGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAGT
5701  GATTGACTACCCGTCAGCGGGGGTCTTTCATT
```

1 - 1457 Mouse mammary tumor virus LTR
1475 - 1726 Double mutated PPE sequence

Figure 9c

1752 - 1754	MN14 heavy chain signal peptide start codon
3156 - 3158	MN14 heavy chain stop codon
3170 - 3745	EMCV IRES
3746 - 3748	Bovine alpha-lactalbumin signal peptide start codon
3803 - 3805	First codon of mature MN14 light chain gene
4442 - 4444	MN14 antibody light chain gene stop codon
4487 - 5078	WPRE sequence
5133 - 5372	MoMuLV 3' LTR

Figure 10a
SEQ ID NO:7
Alpha-Lactalbumin MN14 Vector

```
1     AAAGACCCCACCCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTTTGCA
51    AGGCATGGAAAAATACATAACTGAGAATAGAAAAGTTCAGATCAAGGTCA
101   GGAACAAAGAAACAGCTGAATACCAAACAGGATATCTGTGGTAAGCGGTT
151   CCTGCCCCGGCTCAGGGCCAAGAACAGATGAGACAGCTGAGTGATGGGCC
201   AAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCGGGGCCAAGAA
251   CAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAATCAT
301   CAGATGTTTCCAGGGTGCCCCAAGGACCTGAAAATGACCCTGTACCTTAT
351   TTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTCCGCT
401   CTCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGCGCGCCAGTCT
451   TCCGATAGACTGCGTCGCCCGGGTACCCGTATTCCCAATAAAGCCTCTTG
501   CTGTTTGCATCCGAATCGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCTCT
551   GAGTGATTGACTACCCACGACGGGGGTCTTTCATTTGGGGGCTCGTCCGG
601   GATTTGGAGACCCCTGCCCAGGGACCACCGACCCACCACCGGGAGGTAAG
651   CTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATGTTTG
701   ATGTTATGCGCCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTATCTGG
751   CGGACCCGTGGTGGAACTGACGAGTTCTGAACACCCGGCCGCAACCCTGG
801   GAGACGTCCCAGGGACTTTGGGGGCCGTTTTTGTGGCCCGACCTGAGGAA
851   GGGAGTCGATGTGGAATCCGACCCCGTCAGGATATGTGGTTCTGGTAGGA
901   GACGAGAACCTAAAACAGTTCCCGCCTCCGTCTGAATTTTTGCTTTCGGT
951   TTGGAACCGAAGCCGCGCGTCTTGTCTGCTGCAGCGCTGCAGCATCGTTC
1001  TGTGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATTAGGGC
1051  CAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAGATGT
1101  CGAGCGGATCGCTCACAACCAGTCGGTAGATGTCAAGAAGAGACGTTGGG
1151  TTACCTTCTGCTCTGCAGAATGGCCAACCTTTAACGTCGGATGGCCGCGA
1201  GACGGCACCTTTAACCGAGACCTCATCACCCAGGTTAAGATCAAGGTCTT
1251  TTCACCTGGCCCGCATGGACACCCAGACCAGGTCCCCTACATCGTGACCT
1301  GGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTACAC
1351  CCTAAGCCTCCGCCTCCTCTTCCTCCATCCGCCCCGTCTCTCCCCCTTGA
1401  ACCTCCTCGTTCGACCCCGCCTCGATCCTCCCTTTATCCAGCCCTCACTC
1451  CTTCTCTAGGCGCCGGAATTCCGATCTGATCAAGAGACAGGATGAGGATC
1501  GTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTT
1551  GGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGC
1601  TCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTT
1651  TGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAGGACGAGGCAG
1701  CGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTC
1751  GACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCC
1801  GGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCA
1851  TCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGC
1901  CCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGAT
1951  GGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGC
2001  TCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGACGGC
2051  GAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGT
2101  GGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGG
2151  CGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAG
2201  CTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGC
2251  TCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCT
2301  GAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGC
2351  CATCACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTC
2401  GGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCT
2451  CATGCTGGAGTTCTTCGCCCACCCCGGGCTCGATCCCCTCGCGAGTTGGT
2501  TCAGCTGCTGCCTGAGGCTGGACGACCTCGCGGAGTTCTACCGGCAGTGC
2551  AAATCCGTCGGCATCCAGGAAACCAGCAGCGGCTATCCGCGCATCCATGC
2601  CCCCGAACTGCAGGAGTGGGGAGGCACGATGGCCGCTTTGGTCGAGGCGG
2651  ATCCTAGAACTAGCGAAAATGCAAGAGCAAAGACGAAAACATGCCACACA
2701  TGAGGAATACCGATTCTCTCATTAACATATTCAGGCCAGTTATCTGGGCT
2751  TAAAAGCAGAAGTCCAACCCAGATAACGATCATATACATGGTTCTCTCCA
2801  GAGGTTCATTACTGAACACTCGTCCGAGAATAACGAGTGGATCAGTCCTG
```

Figure 10b

```
2851 GGTGGTCATTGAAAGGACTGATGCTGAAGTTGAAGCTCCAATACTTTGGC
2901 CACCTGATGCGAAGAACTGACTCATGTGATAAGACCCTGATACTGGGAAA
2951 GATTGAAGGCAGGAGGAGAAGGGATGACAGAGGATGGAAGAGTTGGATGG
3001 AATCACCAACTCGATGGACATGAGTTTGAGCAAGCTTCCAGGAGTTGGTA
3051 ATGGGCAGGGAAGCCTGGCGTGCTGCAGTCCATGGGGTTGCAAAGAGTTG
3101 GACACTACTGAGTGACTGAACTGAACTGATAGTGTAATCCATGGTACAGA
3151 ATATAGGATAAAAAGAGGAAGAGTTTGCCCTGATTCTGAAGAGTTGTAG
3201 GATATAAAAGTTTAGAATACCTTTAGTTTGGAAGTCTTAAATTATTTACT
3251 TAGGATGGGTACCCACTGCAATATAAGAAATCAGGCTTTAGAGACTGATG
3301 TAGAGAGAATGAGCCCTGGCATACCAGAAGCTAACAGCTATTGGTTATAG
3351 CTGTTATAACCAATATATAACCAATATATTGGTTATATAGCATGAAGCTT
3401 GATGCCAGCAATTTGAAGGAACCATTTAGAACTAGTATCCTAAACTCTAC
3451 ATGTTCCAGGACACTGATCTTAAAGCTCAGGTTCAGAATCTTGTTTTATA
3501 GGCTCTAGGTGTATATTGTGGGGCTTCCCTGGTGGCTCAGATGGTAAAGT
3551 GTCTGCCTGCAATGTGGGTGATCTGGGTTCGATCCCTGGCTTGGGAAGAT
3601 CCCCTGGAGAAGGAAATGGCAACCCACTCTAGTACTCTTACCTGGAAAAT
3651 TCCATGGACAGAGGAGCCTTGTAAGCTACAGTCCATGGGATTGCAAAGAG
3701 TTGAACACAACTGAGCAACTAAGCACAGCACAGTACAGTATACACCTGTG
3751 AGGTGAAGTGAAGTGAAGGTTCAATGCAGGGTCTCCTGCATTGCAGAAAG
3801 ATTCTTTACCATCTGAGCCACCAGGGAAGCCCAAGAATACTGGAGTGGGT
3851 AGCCTATTCCTTCTCCAGGGGATCTTCCCATCCCAGGAATTGAACTGGAG
3901 TCTCCTGCATTTCAGGTGGATTCTTCACCAGCTGAACTACCAGGTGGATA
3951 CTACTCCAATATTAAAGTGCTTAAAGTCCAGTTTTCCCACCTTTCCCAAA
4001 AAGGTTGGGTCACTCTTTTTTAACCTTCTGTGGCCTACTCTGAGGCTGTC
4051 TACAAGCTTATATATTTATGAACACATTTATTGCAAGTTGTTAGTTTTAG
4101 ATTTACAATGTGGTATCTGGCTATTTAGTGGTATTGGTGGTTGGGGATGG
4151 GGAGGCTGATAGCATCTCAGAGGGCAGCTAGATACTGTCATACACACTTT
4201 TCAAGTTCTCCATTTTTGTGAAATAGAAAGTCTCTGGATCTAAGTTATAT
4251 GTGATTCTCAGTCTCTGTGGTCATATTCTATTCTACTCCTGACCACTCAA
4301 CAAGGAACCAAGATATCAAGGGACACTTGTTTTGTTTCATGCCTGGGTTG
4351 AGTGGGCCATGACATATGTTCTGGGCCTTGTTACATGGCTGGATTGGTTG
4401 GACAAGTGCCAGCTCTGATCCTGGGACTGTGGCATGTGATGACATACACC
4451 CCCTCTCCACATTCTGCATGTCTCTAGGGGGGAAGGGGGAAGCTCGGTAT
4501 AGAACCTTTATTGTATTTTCTGATTGCCTCACTTCTTATATTGCCCCCAT
4551 GCCCTTCTTTGTTCCTCAAGTAACCAGAGACAGTGCTTCCCAGAACCAAC
4601 CCTACAAGAAACAAAGGGCTAAACAAAGCCAAATGGGAAGCAGGATCATG
4651 GTTTGAACTCTTTCTGGCCAGAGAACAATACCTGCTATGGACTAGATACT
4701 GGGAGAGGGAAAGGAAAAGTAGGGTGAATTATGGAAGGAAGCTGGCAGGC
4751 TCAGCGTTTCTGTCTTGGCATGACCAGTCTCTCTTCATTCTCTTCCTAGA
4801 TGTAGGGCTTGGTACCAGAGCCCCTGAGGCTTTCTGCATGAATATAAATA
4851 TATGAAACTGAGTGATGCTTCCATTTCAGGTTCTTGGGGGCGCCGAATTC
4901 GAGCTCGGTACCCGGGGATCTCGACGGATCCGATTACTTACTGGCAGGTG
4951 CTGGGGGCTTCCGAGACAATCGCGAACATCTACACCACACAACACCGCCT
5001 CGACCAGGGTGAGATATCGGCCGGGGACGCGGCGGTGGTAATTACAAGCG
5051 AGATCCGATTACTTACTGGCAGGTGCTGGGGGCTTCCGAGACAATCGCGA
5101 ACATCTACACCACACAACACCGCCTCGACCAGGGTGAGATATCGGCCGGG
5151 GACGCGGCGGTGGTAATTACAAGCGAGATCCCCGGGAATTCAGGACCTCA
5201 CCATGGGATGGAGCTGTATCATCCTCTTCTTGGTAGCAACAGCTACAGGT
5251 GTCCACTCCGAGGTCCAACTGGTGGAGAGCGGTGGAGGTGTTGTGCAACC
5301 TGGCCGGTCCCTGCGCCTGTCCTGCTCCGCATCTGGCTTCGATTTCACCA
5351 CATATTGGATGAGTTGGGTGAGACAGGCACCTGGAAAAGGTCTTGAGTGG
5401 ATTGGAGAAATTCATCCAGATAGCAGTACGATTAACTATGCGCCGTCTCT
5451 AAAGGATAGATTTACAATATCGCGAGACAACGCCAAGAACACATTGTTCC
5501 TGCAAATGGACAGCCTGAGACCCGAAGACACCGGGGTCTATTTTTGTGCA
5551 AGCCTTTACTTCGGCTTCCCCTGGTTTGCTTATTGGGGCCAAGGGACCCC
5601 GGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGG
5651 CACCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTG
5701 GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACTCAGGCGC
5751 CCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGGAC
5801 TCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACC
5851 CAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGA
5901 CAAGAGAGTTGAGCCCAAATCTTGTGACAAAACTCACACATGCCCACCGT
```

Figure 10c

5951 GCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCCTCTTCCCCCCA
6001 AAACCCAAGGACACCCTCATGATCTCCCGGACCCCTGAGGTCACATGCGT
6051 GGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACG
6101 TGGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAG
6151 TACAACAGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGA
6201 CTGGCTGAATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCC
6251 CAGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAA
6301 CCACAGGTGTACACCCTGCCCCCATCCCGGGAGGAGATGACCAAGAACCA
6351 GGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCG
6401 TGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCT
6451 CCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTATAGCAAGCTCACCGT
6501 GGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGC
6551 ACGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCC
6601 GGGAAATGAAAGCCGAATTCGCCCCTCTCCCTCCCCCCCCCCTAACGTTA
6651 CTGGCCGAAGCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTA
6701 TTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGG
6751 CCCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAG
6801 GAATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCT
6851 TCTTGAAGACAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCC
6901 CCCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATA
6951 CACCTGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTT
7001 GTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAA
7051 GGATGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGT
7101 GCACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCC
7151 CCGAACCACGGGGACGTGGTTTTCCTTTGAAAAACACGATGATAATATGG
7201 CCTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAG
7251 GCCGACATCCAGCTGACCCAGAGCCCAAGCAGCCTGAGCGCCAGCGTGGG
7301 TGACAGAGTGACCATCACCTGTAAGGCCAGTCAGGATGTGGGTACTTCTG
7351 TAGCCTGGTACCAGCAGAAGCCAGGTAAGGCTCCAAAGCTGCTGATCTAC
7401 TGGACATCCACCCGGCACACTGGTGTGCCAAGCAGATTCAGCGGTAGCGG
7451 TAGCGGTACCGACTTCACCTTCACCATCAGCAGCCTCCAGCCAGAGGACA
7501 TCGCCACCTACTACTGCCAGCAATATAGCCTCTATCGGTCGTTCGGCCAA
7551 GGGACCAAGGTGGAAATCAAACGAACTGTGGCTGCACCATCTGTCTTCAT
7601 CTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTGCCTCTGTTGTGT
7651 GCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTG
7701 GATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAGCAGGA
7751 CAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAG
7801 CAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGC
7851 CTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGAGATC
7901 CCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATAATCAACCTCTGG
7951 ATTACAAAATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCT
8001 TTTACGCTATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGC
8051 TTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTGCTGT
8101 CTCTTTATGAGGAGTTGTGGCCCGTTGTCAGGCAACGTGGCGTGGTGTGC
8151 ACTGTGTTTGCTGACGCAACCCCCACTGGTTGGGGCATTGCCACCACCTG
8201 TCAGCTCCTTTCCGGGACTTTCGCTTTCCCCCTCCCTATTGCCACGGCGG
8251 AACTCATCGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTG
8301 GGCACTGACAATTCCGTGGTGTTGTCGGGGAAATCATCGTCCTTTCCTTG
8351 GCTGCTCGCCTGTGTTGCCACCTGGATTCTGCGCGGGACGTCCTTCTGCT
8401 ACGTCCCTTCGGCCCTCAATCCAGCGGACCTTCCTTCCCGCGGCCTGCTG
8451 CCGGCTCTGCGGCCTCTTCCGCGTCTTCGCCTTCGCCCTCAGACGAGTCG
8501 GATCTCCCTTTGGGCCGCCTCCCCGCCTGATCGATACCGTCAACATCGAT
8551 AAAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAATGAAAGACC
8601 CCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCA
8651 TGGAAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGGTCAGGAAC
8701 AGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTT
8751 CCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCA
8801 AACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAAC
8851 AGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATC
8901 AGATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTT
8951 GAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTCTGCTCC
9001 CCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGCCAGTCCTC

Figure 10d

```
9051   CGATTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACCCTCTTGCA
9101   GTTGCATCCGACTTGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAG
9151   TGATTGACTACCCGTCAGCGGGGGTCTTTCATT
```

1 - 658	MoMuSV 5' LTR
659 - 1468	Extended packaging region
1512 - 2306	Neomycin resistance gene
2661 - 4896	Bovine/human alpha-lactalbumin 5' flanking region
5084 - 5327	Double mutated PPE sequence
6207 - 6209	MN14 antibody heavy chain gene signal peptide start codon
6611-6613	MN14 antibody heavy chain stop codon
6625 - 7200	EMCV IRES
7201 - 7203	Bovine alpha-lactalbumin signal peptide start codon
7258 - 7260	First codon of mature MN14 antibody light chain gene
7897 - 7899	MN14 antibody light gene stop codon
7938 - 8529	WPRE sequence
8600 - 9138	Moloney murine leukemia virus 3' LTR

Figure 11a
SEQ ID NO:8
Alpha-Lactalbumin Bot Vector

1 GATCAGTCCTGGGTGGTCATTGAAAGGACTGATGCTGAAGTTGAAGCTCC
51 AATACTTTGGCCACCTGATGCGAAGAACTGACTCATGTGATAAGACCCTG
101 ATACTGGGAAAGATTGAAGGCAGGAGGAGAAGGGATGACAGAGGATGGAA
151 GAGTTGGATGGAATCACCAACTCGATGGACATGAGTTTGAGCAAGCTTCC
201 AGGAGTTGGTAATGGGCAGGGAAGCCTGGCGTGCTGCAGTCCATGGGGTT
251 GCAAAGAGTTGGACACTACTGAGTGACTGAACTGAACTGATAGTGTAATC
301 CATGGTACAGAATATAGGATAAAAAAGAGGAAGAGTTTGCCCTGATTCTG
351 AAGAGTTGTAGGATATAAAAGTTTAGAATACCTTTAGTTTGGAAGTCTTA
401 AATTATTTACTTAGGATGGGTACCCACTGCAATATAAGAAATCAGGCTTT
451 AGAGACTGATGTAGAGAGAATGAGCCCTGGCATACCAGAAGCTAACAGCT
501 ATTGGTTATAGCTGTTATAACCAATATATAACCAATATATTGGTTATATA
551 GCATGAAGCTTGATGCCAGCAATTTGAAGGAACCATTTAGAACTAGTATC
601 CTAAACTCTACATGTTCCAGGACACTGATCTTAAAGCTCAGGTTCAGAAT
651 CTTGTTTTATAGGCTCTAGGTGTATATTGTGGGGCTTCCCTGGTGGCTCA
701 GATGGTAAAGTGTCTGCCTGCAATGTGGGTGATCTGGGTTCGATCCCTGG
751 CTTGGGAAGATCCCCTGGAGAAGGAAATGGCAACCCACTCTAGTACTCTT
801 ACCTGGAAAATTCCATGGACAGAGGAGCCTTGTAAGCTACAGTCCATGGG
851 ATTGCAAAGAGTTGAACACAACTGAGCAACTAAGCACAGCACAGTACAGT
901 ATACACCTGTGAGGTGAAGTGAAGTGAAGGTTCAATGCAGGGTCTCCTGC
951 ATTGCAGAAAGATTCTTTACCATCTGAGCCACCAGGGAAGCCCAAGAATA
1001 CTGGAGTGGGTAGCCTATTCCTTCTCCAGGGGATCTTCCCATCCCAGGAA
1051 TTGAACTGGAGTCTCCTGCATTTCAGGTGGATTCTTCACCAGCTGAACTA
1101 CCAGGTGGATACTACTCCAATATTAAAGTGCTTAAAGTCCAGTTTTCCCA
1151 CCTTTCCCAAAAAGGTTGGGTCACTCTTTTTTAACCTTCTGTGGCCTACT
1201 CTGAGGCTGTCTACAAGCTTATATATTTATGAACACATTTATTGCAAGTT
1251 GTTAGTTTTAGATTTACAATGTGGTATCTGGCTATTTAGTGGTATTGGTG
1301 GTTGGGGATGGGGAGGCTGATAGCATCTCAGAGGGCAGCTAGATACTGTC
1351 ATACACACTTTTCAAGTTCTCCATTTTTGTGAAATAGAAAGTCTCTGGAT
1401 CTAAGTTATATGTGATTCTCAGTCTCTGTGGTCATATTCTATTCTACTCC
1451 TGACCACTCAACAAGGAACCAAGATATCAAGGGACACTTGTTTTGTTTCA
1501 TGCCTGGGTTGAGTGGGCCATGACATATGTTCTGGGCCTTGTTACATGGC
1551 TGGATTGGTTGGACAAGTGCCAGCTCTGATCCTGGGACTGTGGCATGTGA
1601 TGACATACACCCCCTCTCCACATTCTGCATGTCTCTAGGGGGGAAGGGGG
1651 AAGCTCGGTATAGAACCTTTATTGTATTTTCTGATTGCCTCACTTCTTAT
1701 ATTGCCCCCATGCCCTTCTTTGTTCCTCAAGTAACCAGAGACAGTGCTTC
1751 CCAGAACCAACCCTACAAGAAACAAAGGGCTAAACAAAGCCAAATGGGAA
1801 GCAGGATCATGGTTTGAACTCTTTCTGGCCAGAGAACAATACCTGCTATG
1851 GACTAGATACTGGGAGAGGGAAAGGAAAAGTAGGGTGAATTATGGAAGGA
1901 AGCTGGCAGGCTCAGCGTTTCTGTCTTGGCATGACCAGTCTCTCTTCATT
1951 CTCTTCCTAGATGTAGGGCTTGGTACCAGAGCCCCTGAGGCTTTCTGCAT
2001 GAATATAAATATATGAAACTGAGTGATGCTTCCATTTCAGGTTCTTGGGG
2051 GCGCCGAATTCGAGCTCGGTACCCGGGGATCTCGACGGATCCGATTACTT
2101 ACTGGCAGGTGCTGGGGGCTTCCGAGACAATCGCGAACATCTACACCACA
2151 CAACACCGCCTCGACCAGGGTGAGATATCGGCCGGGGACGCGGCGGTGGT
2201 AATTACAAGCGAGATCCGATTACTTACTGGCAGGTGCTGGGGGCTTCCGA
2251 GACAATCGCGAACATCTACACCACACAACACCGCCTCGACCAGGGTGAGA
2301 TATCGGCCGGGGACGCGGCGGTGGTAATTACAAGCGAGATCTCGAGAAGC
2351 TTGTTGGGAATTCAGGCCATCGATCCCGCCGCCACCATGGAATGGAGCTG
2401 GGTCTTTCTCTTCTTCCTGTCAGTAACTACAGGTGTCCACTCCGACATCC
2451 AGATGACCCAGTCTCCAGCCTCCCTATCTGCATCTGTGGGAGAAACTGTC
2501 ACTATCACATGTCGAGCAAGTGGGAATATTCACAATTATTTAGCATGGTA
2551 TCAGCAGAAACAGGGAAAATCTCCTCAGCTCCTGGTCTATAATGCAAAAA
2601 CCTTAGCAGATGGTGTGCCATCAAGGTTCAGTGGCAGTGGATCAGGAACA
2651 CAATATTCTCTCAAGATCAACAGCCTGCAGCCTGAAGATTTTGGGAGTTA
2701 TTACTGTCAACATTTTTGGAGTACTCCGTGGACGTTCGGTGGAGGCACCA
2751 AGCTGGAAATCAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCA
2801 CCATCCAGTGAGCAGTTAACATCTGGAGGTGCCTCAGTCGTGTGCTTCTT

Figure 11b

2851 GAACAACTTCTACCCCAAAGACATCAATGTCAAGTGGAAGATTGATGGCA
2901 GTGAACGACAAAATGGCGTCCTGAACAGTTGGACTGATCAGGACAGCAAA
2951 GACAGCACCTACAGCATGAGCAGCACCCTCACATTGACCAAGGACGAGTA
3001 TGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTT
3051 CACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTGAAAGCATCGATTT
3101 CCCCTGAATTCGCCCCTCTCCCTCCCCCCCCCCTAACGTTACTGGCCGAA
3151 GCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTTCCACC
3201 ATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGTCTT
3251 CTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGAATGCAAG
3301 GTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGA
3351 CAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGG
3401 CGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAA
3451 AGGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGA
3501 GTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCA
3551 GAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCT
3601 TTACATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCCCCGAACCAC
3651 GGGGACGTGGTTTTCCTTTGAAAAACACGATGATAATATGGCCTCCTTTG
3701 TCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCCGAGGTT
3751 CAGCTTCAGCAGTCTGGGGCAGAGCTTGTGAAGCCAGGGGCCTCAGTCAA
3801 GTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACACCTTTATGCACT
3851 GGGTGAAGCAGAGGCCTGAACAGGGCCTGGAGTGGATTGGAAGGATTGAT
3901 CCTGCGAATGGGAATACTGAATATGACCCGAAGTTCCAGGGCAAGGCCAC
3951 TATAACAGCAGACACATCCTCCAACACAGTCAACCTGCAGCTCAGCAGCC
4001 TGACATCTGAGGACACTGCCGTCTATTACTGTGCTAGTGGAGGGGAACTG
4051 GGGTTTCCTTACTGGGGCCAAGGGACTCTGGTCACTGTCTCTGCAGCCAA
4101 AACGACACCCCCATCTGTCTATCCACTGGCCCCTGGATCTGCTGCCCAAA
4151 CTAACTCCATGGTGACCCTGGGATGCCTGGTCAAGGGCTATTTCCCTGAG
4201 CCAGTGACAGTGACCTGGAACTCTGGATCCCTGTCCAGCGGTGTGCACAC
4251 CTTCCCAGCTGTCCTGCAGTTTGACCTCTACACTCTGAGCAGCTCAGTGA
4301 CTGTCCCCTCCAGCACCTGGCCCAGCGAGACCGTCACCTGCAACGTTGCC
4351 CACCCGGCCAGCAGCACCAAGGTGGACAAGAAAATTGTGCCCAGGGATTG
4401 TACTAGTGGAGGTGGAGGTAGCCACCATCACCATCACCATTAATCTAGAG
4451 TTAAGCGGCCGTCGAGATCTCGACATCGATAATCAACCTCTGGATTACAA
4501 AATTTGTGAAAGATTGACTGGTATTCTTAACTATGTTGCTCCTTTTACGC
4551 TATGTGGATACGCTGCTTTAATGCCTTTGTATCATGCTATTGCTTCCCGT
4601 ATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTGCTGTCTCTTTA
4651 TGAGGAGTTGTGGCCCGTTGTCAGGCAACGTGGCGTGGTGTGCACTGTGT
4701 TTGCTGACGCAACCCCCACTGGTTGGGGCATTGCCACCACCTGTCAGCTC
4751 CTTTCCGGGACTTTCGCTTTCCCCCTCCCTATTGCCACGGCGGAACTCAT
4801 CGCCGCCTGCCTTGCCCGCTGCTGGACAGGGGCTCGGCTGTTGGGCACTG
4851 ACAATTCCGTGGTGTTGTCGGGGAAATCATCGTCCTTTCCTTGGCTGCTC
4901 GCCTGTGTTGCCACCTGGATTCTGCGCGGGACGTCCTTCTGCTACGTCCC
4951 TTCGGCCCTCAATCCAGCGGACCTTCCTTCCCGCGGCCTGCTGCCGGCTC
5001 TGCGGCCTCTTCCGCGTCTTCGCCTTCGCCCTCAGACGAGTCGGATCTCC
5051 CTTTGGGCCGCCTCCCCGCCTGATCGATAAAATAAAAGATTTTATTTAGT
5101 CTCCAGAAAAAGGGGGGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCT
5151 AGCTTAAGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTGAGAA
5201 TAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGG
5251 CCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAG
5301 AACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCA
5351 GTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCC
5401 AGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAA
5451 GGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTT
5501 CTCGCTTCTGTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCA
5551 CAACCCCTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCCGGGT
5601 ACCCGTGTATCCAATAAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTC

Figure 11c

5651 GCTGTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGG
5701 GGTCTTTCATT

1 - 2053	Bovine/human alpha-lactalbumin 5' flanking region
2093 - 2336	Double mtated PPE sequence
2387 - 2443	cc49 signal peptide coding region
2444 - 3088	Bot antibody light chain Fab coding region
3112 - 3686	EMCV IRES
3687 - 3745	Bovine alpha-lactalbumin signal peptide coding region
3746 - 4443	Bot antibody heavy chain Fab coding region
4481 - 5072	WPRE sequence
5118 - 5711	Moloney murine leukemia virus 3' LTR

Figure 12a
SEQ ID NO:9
LSNRL Vector

1 TTTGAAAGACCCCACCCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTT
51 TGCAAGGCATGGAAAAATACATAACTGAGAATAGAAAAGTTCAGATCAAG
101 GTCAGGAACAAAGAAACAGCTGAATACCAAACAGGATATCTGTGGTAAGC
151 GGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGAGACAGCTGAGTGATG
201 GGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCGGGGCCA
251 AGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAA
301 TCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAAATGACCCTGTACC
351 TTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTC
401 CGCTCTCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGCGCGCCA
451 GTCTTCCGATAGACTGCGTCGCCCGGGTACCCGTATTCCCAATAAAGCCT
501 CTTGCTGTTTGCATCCGAATCGTGGTCTCGCTGTTCCTTGGGAGGGTCTC
551 CTCTGAGTGATTGACTACCCACGACGGGGGTCTTTCATTTGGGGGCTCGT
601 CCGGGATTTGGAGACCCCTGCCCAGGGACCACCGACCCACCACCGGGAGG
651 TAAGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATG
701 TTTGATGTTATGCGCCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTAT
751 CTGGCGGACCCGTGGTGGAACTGACGAGTTCTGAACACCCGGCCGCAACC
801 CTGGGAGACGTCCCAGGGACTTTGGGGGCCGTTTTTGTGGCCCGACCTGA
851 GGAAGGGAGTCGATGTGGAATCCGACCCCGTCAGGATATGTGGTTCTGGT
901 AGGAGACGAGAACCTAAAACAGTTCCCGCCTCCGTCTGAATTTTTGCTTT
951 CGGTTTGGAACCGAAGCCGCGCGTCTTGTCTGCTGCAGCCAAGCTTGGGC
1001 TGCAGGTCGAGGACTGGGGACCCTGCACCGAACATGGAGAACACAACATC
1051 AGGATTCCTAGGACCCCTGCTCGTGTTACAGGCGGGGTTTTTCTTGTTGA
1101 CAAGAATCCTCACAATACCACAGAGTCTAGACTCGTGGTGGACTTCTCTC
1151 AATTTTCTAGGGGGAGCACCCACGTGTCCTGGCCAAAATTCGCAGTCCCC
1201 AACCTCCAATCACTCACCAACCTCTTGTCCTCCAATTTGTCCTGGCTATC
1251 GCTGGATGTGTCTGCGGCGTTTTATCATATTCCTCTTCATCCTGCTGCTA
1301 TGCCTCATCTTCTTGTTGGTTCTTCTGGACTACCAAGGTATGTTGCCCGT
1351 TTGTCCTCTACTTCCAGGAACATCAACTACCAGCACGGGACCATGCAAGA
1401 CCTGCACGATTCCTGCTCAAGGAACCTCTATGTTTCCCTCTTGTTGCTGT
1451 ACAAAACCTTCGGACGGAAACTGCACTTGTATTCCCATCCCATCATCCTG
1501 GGCTTTCGCAAGATTCCTATGGGAGTGGGCCTCAGTCCGTTTCTCCTGGC
1551 TCAGTTTACTAGTGCCATTTGTTCAGTGGTTCGTAGGGCTTTCCCCCACT
1601 GTTTGGCTTTCAGTTATATGGATGATGTGGTATTGGGGGCCAAGTCTGTA
1651 CAACATCTTGAGTCCCTTTTTACCTCTATTACCAATTTTCTTTTGTCTTT
1701 GGGTATACATTTAAACCCTAATAAAACCAAACGTTGGGGCTACTCCCTTA
1751 ACTTCATGGGATATGTAATTGGATGTTGGGGTACTTTACCGCAAGAACAT
1801 ATTGTACTAAAAATCAAGCAATGTTTTCGAAAACTGCCTGTAAATAGACC
1851 TATTGATTGGAAAGTATGTCAGAGACTTGTGGGTCTTTTGGGCTTTGCTG
1901 CCCCTTTTACACAATGTGGCTATCCTGCCTTAATGCCTTTATATGCATGT
1951 ATACAATCTAAGCAGGCTTTCACTTTCTCGCCAACTTACAAGGCCTTTCT
2001 GTGTAAACAATATCTGAACCTTTACCCCGTTGCCCGGCAACGGTCAGGTC
2051 TCTGCCAAGTGTTTGCTGACGCAACCCCCACTGGATGGGGCTTGGCTATC
2101 GGCCATAGCCGCATGCGCGGACCTTTGTGGCTCCTCTGCCGATCCATACT
2151 GCGGAACTCCTAGCAGCTTGTTTTGCTCGCAGGCGGTCTGGAGCGAAACT
2201 TATCGGCACCGACAACTCTGTTGTCCTCTCTCGGAAATACACCTCCTTTC
2251 CATGGCTGCTAGGGTGTGCTGCCAACTGGATCCCCTCAGGATATAGTAGT
2301 TTCGCTTTTGCATAGGGAGGGGGAAATGTAGTCTTATGCAATACACTTGT
2351 AGTCTTGCAACATGGTAACGATGAGTTAGCAACATGCCTTACAAGGAGAG
2401 AAAAAGCACCGTGCATGCCGATTGGTGGAAGTAAGGTGGTACGATCGTGC
2451 CTTATTAGGAAGGCAACAGACAGGTCTGACATGGATTGGACGAACCACTG
2501 AATTCCGCATTGCAGAGATAATTGTATTTAAGTGCCTAGCTCGATACAGC
2551 AAACGCCATTTTTGACCATTCACCACATTGGTGTGCACCTTCCAAAGCTT
2601 CACGCTGCCGCAAGCACTCAGGGCGCAAGGGCTGCTAAAGGAAGCGGAAC
2651 ACGTAGAAAGCCAGTCCGCAGAAACGGTGCTGACCCCGGATGAATGTCAG
2701 CTACTGGGCTATCTGGACAAGGGAAAACGCAAGCGCAAAGAGAAAGCAGG
2751 TAGCTTGCAGTGGGCTTACATGGCGATAGCTAGACTGGGCGGTTTTATGG
2801 ACAGCAAGCGAACCGGAATTGCCAGCTGGGGCGCCCTCTGGTAAGGTTGG

Figure 12b

```
2851  GAAGCCCTGCAAAGTAAACTGGATGGCTTTCTTGCCGCCAAGGATCTGAT
2901  GGCGCAGGGGATCAAGATCTGATCAAGAGACAGGATGAGGATCGTTTCGC
2951  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGA
3001  GAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATG
3051  CCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAG
3101  ACCGACCTGTCCGGTGCCCTGAATGAACTGCAGGACGAGGCAGCGCGGCT
3151  ATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTG
3201  TCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG
3251  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGC
3301  TGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCG
3351  ACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCC
3401  GGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCC
3451  AGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGACGGCGAGGATC
3501  TCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT
3551  GGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCG
3601  CTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCG
3651  GCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGAT
3701  TCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGG
3751  ACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACG
3801  AGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCG
3851  TTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTG
3901  GAGTTCTTCGCCCACCCCAACCCTGGCCCTATTATTGGGTGGACTAACCA
3951  TGGGGGGAATTGCCGCTGGAATAGGAACAGGGACTACTGCTCTAATGGCC
4001  ACTCAGCAATTCCAGCAGCTCCAAGCCGCAGTACAGGATGATCTCAGGGA
4051  GGTTGAAAAATCAATCTCTAACCTAGAAAAGTCTCTCACTTCCCTGTCTG
4101  AAGTTGTCCTACAGAATCGAAGGGGCCTAGACTTGTTATTTCTAAAAGAA
4151  GGAGGGCTGTGTGCTGCTCTAAAAGAAGAATGTTGCTTCTATGCGGACCA
4201  CACAGGACTAGTGAGAGACAGCATGGCCAAATTGAGAGAGAGGCTTAATC
4251  AGAGACAGAAACTGTTTGAGTCAACTCAAGGATGGTTTGAGGGACTGTTT
4301  AACAGATCCCCTTGGTTTACCACCTTGATATCTACCATTATGGGACCCCT
4351  CATTGTACTCCTAATGATTTTGCTCTTCGGACCCTGCATTCTTAATCGAT
4401  TAGTCCAATTTGTTAAAGACAGGATATCAGTGGTCCAGGCTCTAGTTTTG
4451  ACTCAACAATATCACCAGCTGAAGCCTATAGAGTACGAGCCATAGATAAA
4501  ATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAATGAAAGACCCCA
4551  CCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCATGG
4601  AAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGGTCAGGAACAGA
4651  TGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCT
4701  GCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAATATGGGCCAAAC
4751  AGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGA
4801  TGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGAGAACCATCAGA
4851  TGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTGCCTTATTTGAA
4901  CTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTCTGCTCCCCG
4951  AGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGCCAGTCCTCCGA
5001  TTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACCCTCTTGCAGTT
5051  GCATCCGACTTGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCTCTGAGTGA
5101  TTGACTACCCGTCAGCGGGGGTCTTTCATT
```

1 - 589	MoMuSV 5' LTR
659 - 897	Retroviral packaging region
1034 - 1714	Hepatitis B surface antigen
2279 - 2595	RSV promoter
2951 - 3745	Neomycin phosphotransferase gene
4537 - 5130	MoMuLV 3' LTR

Figure 13a
SEQ ID NO:10
Alpha-Lactalbumin cc49IL2 Vector

```
1     GATCAGTCCTGGGTGGTCATTGAAAGGACTGATGCTGAAGTTGAAGCTCC
51    AATACTTTGGCCACCTGATGCGAAGAACTGACTCATGTGATAAGACCCTG
101   ATACTGGGAAAGATTGAAGGCAGGAGGAGAAGGGATGACAGAGGATGGAA
151   GAGTTGGATGGAATCACCAACTCGATGGACATGAGTTTGAGCAAGCTTCC
201   AGGAGTTGGTAATGGGCAGGGAAGCCTGGCGTGCTGCAGTCCATGGGGTT
251   GCAAAGAGTTGGACACTACTGAGTGACTGAACTGAACTGATAGTGTAATC
301   CATGGTACAGAATATAGGATAAAAAAGAGGAAGAGTTTGCCCTGATTCTG
351   AAGAGTTGTAGGATATAAAAGTTTAGAATACCTTTAGTTTGGAAGTCTTA
401   AATTATTTACTTAGGATGGGTACCCACTGCAATATAAGAAATCAGGCTTT
451   AGAGACTGATGTAGAGAGAATGAGCCCTGGCATACCAGAAGCTAACAGCT
501   ATTGGTTATAGCTGTTATAACCAATATATAACCAATATATTGGTTATATA
551   GCATGAAGCTTGATGCCAGCAATTTGAAGGAACCATTTAGAACTAGTATC
601   CTAAACTCTACATGTTCCAGGACACTGATCTTAAAGCTCAGGTTCAGAAT
651   CTTGTTTTATAGGCTCTAGGTGTATATTGTGGGGCTTCCCTGGTGGCTCA
701   GATGGTAAAGTGTCTGCCTGCAATGTGGGTGATCTGGGTTCGATCCCTGG
751   CTTGGGAAGATCCCCTGGAGAAGGAAATGGCAACCCACTCTAGTACTCTT
801   ACCTGGAAAATTCCATGGACAGAGGAGCCTTGTAAGCTACAGTCCATGGG
851   ATTGCAAAGAGTTGAACACAACTGAGCAACTAAGCACAGCACAGTACAGT
901   ATACACCTGTGAGGTGAAGTGAAGTGAAGGTTCAATGCAGGGTCTCCTGC
951   ATTGCAGAAAGATTCTTTACCATCTGAGCCACCAGGGAAGCCCAAGAATA
1001  CTGGAGTGGGTAGCCTATTCCTTCTCCAGGGGATCTTCCCATCCCAGGAA
1051  TTGAACTGGAGTCTCCTGCATTTCAGGTGGATTCTTCACCAGCTGAACTA
1101  CCAGGTGGATACTACTCCAATATTAAAGTGCTTAAAGTCCAGTTTTCCCA
1151  CCTTTCCCAAAAAGGTTGGGTCACTCTTTTTTAACCTTCTGTGGCCTACT
1201  CTGAGGCTGTCTACAAGCTTATATATTTATGAACACATTTATTGCAAGTT
1251  GTTAGTTTTAGATTTACAATGTGGTATCTGGCTATTTAGTGGTATTGGTG
1301  GTTGGGGATGGGGAGGCTGATAGCATCTCAGAGGGCAGCTAGATACTGTC
1351  ATACACACTTTTCAAGTTCTCCATTTTTGTGAAATAGAAAGTCTCTGGAT
1401  CTAAGTTATATGTGATTCTCAGTCTCTGTGGTCATATTCTATTCTACTCC
1451  TGACCACTCAACAAGGAACCAAGATATCAAGGGACACTTGTTTTGTTTCA
1501  TGCCTGGGTTGAGTGGGCCATGACATATGTTCTGGGCCTTGTTACATGGC
1551  TGGATTGGTTGGACAAGTGCCAGCTCTGATCCTGGGACTGTGGCATGTGA
1601  TGACATACACCCCCTCTCCACATTCTGCATGTCTCTAGGGGGGAAGGGGG
1651  AAGCTCGGTATAGAACCTTTATTGTATTTTCTGATTGCCTCACTTCTTAT
1701  ATTGCCCCCATGCCCTTCTTTGTTCCTCAAGTAACCAGAGACAGTGCTTC
1751  CCAGAACCAACCCTACAAGAAACAAAGGGCTAAACAAAGCCAAATGGGAA
1801  GCAGGATCATGGTTTGAACTCTTTCTGGCCAGAGAACAATACCTGCTATG
1851  GACTAGATACTGGGAGAGGGAAAGGAAAAGTAGGGTGAATTATGGAAGGA
1901  AGCTGGCAGGCTCAGCGTTTCTGTCTTGGCATGACCAGTCTCTCTTCATT
1951  CTCTTCCTAGATGTAGGGCTTGGTACCAGAGCCCCTGAGGCTTTCTGCAT
2001  GAATATAAATATATGAAACTGAGTGATGCTTCCATTTCAGGTTCTTGGGG
2051  GCGCCGAATTCGAGCTCGGTACCCGGGGATCTCGAGAAGCTTTAACCATG
2101  GAATGGAGCTGGGTCTTTCTCTTCTTCCTGTCAGTAACTACAGGTGTCCA
2151  CTCCCAGGTTCAGTTGCAGCAGTCTGACGCTGAGTTGGTGAAACCTGGGG
2201  CTTCAGTGAAGATTTCCTGCAAGGCTTCTGGCTACACCTTCACTGACCAT
2251  GCAATTCACTGGGTGAAACAGAACCCTGAACAGGGCCTGGAATGGATTGG
2301  ATATTTTTCTCCCGGAAATGATGATTTTAAATACAATGAGAGGTTCAAGG
2351  GCAAGGCCACACTGACTGCAGACAAATCCTCCAGCACTGCCTACGTGCAG
2401  CTCAACAGCCTGACATCTGAGGATTCTGCAGTGTATTTCTGTACAAGATC
2451  CCTGAATATGGCCTACTGGGGTCAAGGAACCTCAGTCACCGTCTCCTCAG
2501  GAGGCGGAGGCAGCGGAGGCGGTGGCTCGGGAGGCGGAGGCTCGGACATT
2551  GTGATGTCACAGTCTCCATCCTCCCTACCTGTGTCAGTTGGCGAGAAGGT
2601  TACTTTGAGCTGCAAGTCCAGTCAGAGCCTTTTATATAGTGGTAATCAAA
2651  AGAACTACTTGGCCTGGTACCAGCAGAAACCAGGGCAGTCTCCTAAACTG
2701  CTGATTTACTGGGCATCCGCTAGGGAATCTGGGGTCCCTGATCGCTTCAC
2751  AGGCAGTGGATCTGGGACAGATTTCACTCTCTCCATCAGCAGTGTGAAGA
2801  CTGAAGACCTGGCAGTTTATTACTGTCAGCAGTATTATAGCTATCCCCTC
```

Figure 13b

```
2851   ACGTTCGGTGCTGGGACCAAGCTGGTGCTGAAACGGGCCGCCGAGCCCAA
2901   ATCTCCTGACAAAACTCACACATGCCCACCGTGCCCAGCACCTGAACTCC
2951   TGGGGGGACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGACACCCTC
3001   ATGATCTCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCA
3051   CGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGC
3101   ATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGT
3151   GTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGA
3201   GTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAA
3251   CCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG
3301   CCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCTGCCT
3351   GGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGAGCAATG
3401   GGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGCTGGACTCCGAC
3451   GGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCA
3501   GCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACC
3551   ACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAGGAGGCGGATCA
3601   GGAGGTGGCGCACCTACTTCAAGTTCTACAAAGAAAACACAGCTACAACT
3651   GGAGCATTTACTGCTGGATTTACAGATGATTTTGAATGGAATTAATAATT
3701   ACAAGAATCCCAAACTCACCAGGATGCTCACATTTAAGTTTTACATGCCC
3751   AAGAAGGCCACAGAACTGAAACATCTTCAGTGTCTAGAAGAAGAACTCAA
3801   ACCTCTGGAGGAAGTGCTAAATTTAGCTCAAAGCAAAAACTTTCACTTAA
3851   GACCCAGGGACTTAATCAGCAATATCAACGTAATAGTTCTGGAACTAAAG
3901   GGATCTGAAACAACATTCATGTGTGAATATGCTGATGAGACAGCAACCAT
3951   TGTAGAATTTCTGAACAGATGGATTACCTTTTGTCAAAGCATCATCTCAA
4001   CACTAACTTGAAGCTTGTTAACATCGATAAAATAAAAGATTTTATTTAGT
4051   CTCCAGAAAAAGGGGGGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCT
4101   AGCTTAAGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTGAGAA
4151   TAGAGAAGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGG
4201   CCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAG
4251   AACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCA
4301   GTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCC
4351   AGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAA
4401   GGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTT
4451   CTCGCTTCTGTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCA
4501   CAACCCCTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCCGGGT
4551   ACCCGTGTATCCAATAAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTC
4601   GCTGTTCCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGG
4651   GGTCTTTCATT
```

1 - 2055	Bovine/human alpha-lactalbumin 5' flanking region
2098 - 4011	cc49-IL2 coding region
4068 - 4661	MoMuLV 3' LTR

Figure 14a
SEQ ID NO:11
Alpha-Lactalbumin YP Vector

```
1     GATCAGTCCTGGGTGGTCATTGAAAGGACTGATGCTGAAGTTGAAGCTCC
51    AATACTTTGGCCACCTGATGCGAAGAACTGACTCATGTGATAAGACCCTG
101   ATACTGGGAAAGATTGAAGGCAGGAGGAGAAGGGATGACAGAGGATGGAA
151   GAGTTGGATGGAATCACCAACTCGATGGACATGAGTTTGAGCAAGCTTCC
201   AGGAGTTGGTAATGGGCAGGGAAGCCTGGCGTGCTGCAGTCCATGGGGTT
251   GCAAAGAGTTGGACACTACTGAGTGACTGAACTGAACTGATAGTGTAATC
301   CATGGTACAGAATATAGGATAAAAAAGAGGAAGAGTTTGCCCTGATTCTG
351   AAGAGTTGTAGGATATAAAAGTTTAGAATACCTTTAGTTTGGAAGTCTTA
401   AATTATTTACTTAGGATGGGTACCCACTGCAATATAAGAAATCAGGCTTT
451   AGAGACTGATGTAGAGAGAATGAGCCCTGGCATACCAGAAGCTAACAGCT
501   ATTGGTTATAGCTGTTATAACCAATATATAACCAATATATTGGTTATATA
551   GCATGAAGCTTGATGCCAGCAATTTGAAGGAACCATTTAGAACTAGTATC
601   CTAAACTCTACATGTTCCAGGACACTGATCTTAAAGCTCAGGTTCAGAAT
651   CTTGTTTTATAGGCTCTAGGTGTATATTGTGGGGCTTCCCTGGTGGCTCA
701   GATGGTAAAGTGTCTGCCTGCAATGTGGGTGATCTGGGTTCGATCCCTGG
751   CTTGGGAAGATCCCCTGGAGAAGGAAATGGCAACCCACTCTAGTACTCTT
801   ACCTGGAAAATTCCATGGACAGAGGAGCCTTGTAAGCTACAGTCCATGGG
851   ATTGCAAAGAGTTGAACACAACTGAGCAACTAAGCACAGCACAGTACAGT
901   ATACACCTGTGAGGTGAAGTGAAGTGAAGGTTCAATGCAGGGTCTCCTGC
951   ATTGCAGAAAGATTCTTTACCATCTGAGCCACCAGGGAAGCCCAAGAATA
1001  CTGGAGTGGGTAGCCTATTCCTTCTCCAGGGGATCTTCCCATCCCAGGAA
1051  TTGAACTGGAGTCTCCTGCATTTCAGGTGGATTCTTCACCAGCTGAACTA
1101  CCAGGTGGATACTACTCCAATATTAAAGTGCTTAAAGTCCAGTTTTCCCA
1151  CCTTTCCCAAAAAGGTTGGGTCACTCTTTTTTAACCTTCTGTGGCCTACT
1201  CTGAGGCTGTCTACAAGCTTATATATTTATGAACACATTTATTGCAAGTT
1251  GTTAGTTTTAGATTTACAATGTGGTATCTGGCTATTTAGTGGTATTGGTG
1301  GTTGGGGATGGGGAGGCTGATAGCATCTCAGAGGGCAGCTAGATACTGTC
1351  ATACACACTTTTCAAGTTCTCCATTTTTGTGAAATAGAAAGTCTCTGGAT
1401  CTAAGTTATATGTGATTCTCAGTCTCTGTGGTCATATTCTATTCTACTCC
1451  TGACCACTCAACAAGGAACCAAGATATCAAGGGACACTTGTTTTGTTTCA
1501  TGCCTGGGTTGAGTGGGCCATGACATATGTTCTGGGCCTTGTTACATGGC
1551  TGGATTGGTTGGACAAGTGCCAGCTCTGATCCTGGGACTGTGGCATGTGA
1601  TGACATACACCCCCTCTCCACATTCTGCATGTCTCTAGGGGGGAAGGGGG
1651  AAGCTCGGTATAGAACCTTTATTGTATTTTCTGATTGCCTCACTTCTTAT
1701  ATTGCCCCCATGCCCTTCTTTGTTCCTCAAGTAACCAGAGACAGTGCTTC
1751  CCAGAACCAACCCTACAAGAAACAAAGGGCTAAACAAAGCCAAATGGGAA
1801  GCAGGATCATGGTTTGAACTCTTTCTGGCCAGAGAACAATACCTGCTATG
1851  GACTAGATACTGGGAGAGGGAAAGGAAAAGTAGGGTGAATTATGGAAGGA
1901  AGCTGGCAGGCTCAGCGTTTCTGTCTTGGCATGACCAGTCTCTCTTCATT
1951  CTCTTCCTAGATGTAGGGCTTGGTACCAGAGCCCCTGAGGCTTTCTGCAT
2001  GAATATAAATATATGAAACTGAGTGATGCTTCCATTTCAGGTTCTTGGGG
2051  GCGCCGAATTCGAGCTCGGTACCCGGGGATCTCGACGGATCCGATTACTT
2101  ACTGGCAGGTGCTGGGGGCTTCCGAGACAATCGCGAACATCTACACCACA
2151  CAACACCGCCTCGACCAGGGTGAGATATCGGCCGGGGACGCGGCGGTGGT
2201  AATTACAAGCGAGATCCGATTACTTACTGGCAGGTGCTGGGGGCTTCCGA
2251  GACAATCGCGAACATCTACACCACACAACACCGCCTCGACCAGGGTGAGA
2301  TATCGGCCGGGGACGCGGCGGTGGTAATTACAAGCGAGATCTCGAGTTAA
2351  CAGATCTAGGCCTCCTAGGTCGACGGATCCCCGGGAATTCGGCGCCGCCA
2401  CCATGATGTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCC
2451  ACCCAGGCCCAGGTCCAACTGCAGCAGTCTGGGCCTGAGCTGGTGAAGCC
2501  TGGGACTTCAGTGAGGATATCCTGCAAGGCTTCTGGCTACACCTTCACAA
2551  GCTACTATTTACACTGGGTGAAGCAGAGGCCTGGACAGGGACTTGAGTGG
2601  ATTGCATGGATTTATCCTGGAAATGTTATTACTACGTACAATGAGAAGTT
2651  CAAGGGCAAGGCCACACTGACTGCAGACAAATCCTCCAGCACAGCCTACA
2701  TGCACCTCAACAGCCTGACCTCTGAGGACTCTGCGGTCTATTTCTGTGCA
2751  AGGGGTGACCATGATCTTGACTACTGGGGCCAAGGCACCACTCTCACAGT
2801  CTCCTCAGCCAAAACGACACCCCCATCTGTCTATCCACTGGCCCCTGGAT
```

Figure 14b

```
2851   CTGCTGCCCAAACTAACTCCATGGTGACCCTGGGATGCCTGGTCAAGGGC
2901   TATTTCCCTGAGCCAGTGACAGTGACCTGGAACTCTGGATCCCTGTCCAG
2951   CGGTGTGCACACCTTCCCAGCTGTCCTGCAGTCTGACCTCTACACTCTGA
3001   GCAGCTCAGTGACTGTCCCCTCCAGCACCTGGCCCAGCGAGACCGTCACC
3051   TGCAACGTTGCCCACCCGGCCAGCAGCACCAAGGTGGACAAGAAAATTGT
3101   GCCCAGGGATTGTACTAGTGGAGGTGGAGGTAGCTAAGGGAGATCTCGAC
3151   GGATCCCCGGGAATTCGCCCCTCTCCCTCCCCCCCCCCTAACGTTACTGG
3201   CCGAAGCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTT
3251   CCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCT
3301   GTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGAAT
3351   GCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTT
3401   GAAGACAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCA
3451   CCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACC
3501   TGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTTGTGG
3551   AAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGAT
3601   GCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGCAC
3651   ATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCCCCGA
3701   ACCACGGGGACGTGGTTTTCCTTTGAAAAACACGATGATAATATGGCCTC
3751   CTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAGGCCG
3801   ACATTGTGCTGACACAATCTCCAGCAATCATGTCTGCATCTCCAGGGGAG
3851   AAGGTCACCATGACCTGCAGTGCCACCTCAAGTGTAAGTTACATACACTG
3901   GTACCAGCAGAAGTCAGGCACCTCCCCCAAAAGATGGATTTATGACACAT
3951   CCAAACTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGG
4001   ACCTCTCACTCTCTCACACTCAGCAGCATGGAGGCTGAAGATGCTGCCAC
4051   TTATTACTGCCAGCAGTGGGGTAGTTACCTCACGTTCGGTGCGGGGACCA
4101   AGCTGGAGCTGAAACGGGCTGATGCTGCACCAACTGTATCCATCTTCCCA
4151   CCATCCAGTGAGCAGTTAACATCTGGAGGTGCCTCAGTCGTGTGCTTCTT
4201   GAACAACTTCTACCCCAAAGACATCAATGTCAAGTGGAAGATTGATGGCA
4251   GTGAACGACAAAATGGCGTCCTGAACAGTTGGACTGATCAGGACAGCAAA
4301   GACAGCACCTACAGCATGAGCAGCACCCTCACGTTGACCAAGGACGAGTA
4351   TGAACGACATAACAGCTATACCTGTGAGGCCACTCACAAGACATCAACTT
4401   CACCCATTGTCAAGAGCTTCAACAGGAATGAGTGTTAATAGGGGAGATCT
4451   CGACATCGATAATCAACCTCTGGATTACAAAATTTGTGAAAGATTGACTG
4501   GTATTCTTAACTATGTTGCTCCTTTTACGCTATGTGGATACGCTGCTTTA
4551   ATGCCTTTGTATCATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTC
4601   CTTGTATAAATCCTGGTTGCTGTCTCTTTATGAGGAGTTGTGGCCCGTTG
4651   TCAGGCAACGTGGCGTGGTGTGCACTGTGTTTGCTGACGCAACCCCCACT
4701   GGTTGGGGCATTGCCACCACCTGTCAGCTCCTTTCCGGGACTTTCGCTTT
4751   CCCCCTCCCTATTGCCACGGCGGAACTCATCGCCGCCTGCCTTGCCCGCT
4801   GCTGGACAGGGGCTCGGCTGTTGGGCACTGACAATTCCGTGGTGTTGTCG
4851   GGGAAATCATCGTCCTTTCCTTGGCTGCTCGCCTGTGTTGCCACCTGGAT
4901   TCTGCGCGGGACGTCCTTCTGCTACGTCCCTTCGGCCCTCAATCCAGCGG
4951   ACCTTCCTTCCCGCGGCCTGCTGCCGGCTCTGCGGCCTCTTCCGCGTCTT
5001   CGCCTTCGCCCTCAGACGAGTCGGATCTCCCTTTGGGCCGCCTCCCCGCC
5051   TGATCGATAAAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGGGGAAT
5101   GAAAGACCCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTT
5151   GCAAGGCATGGAAAAATACATAACTGAGAATAGAGAAGTTCAGATCAAGG
5201   TCAGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGT
5251   AAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGCTGAAT
5301   ATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGG
5351   CCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGA
5401   GAACCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACCCTGTG
5451   CCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCT
5501   TCTGCTCCCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGGGCGC
5551   CAGTCCTCCGATTGACTGAGTCGCCCGGGTACCCGTGTATCCAATAAACC
5601   CTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTTCCTTGGGAGGGTCT
```

Figure 14c

5651 CCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTTTCATT

1 - 2053	Bovine/Human Alpha-lactalbumin 5' flanking region
2093 - 2336	Double mutated PPE sequence
2403 - 2459	Bovine alpha-lactalbumin signal peptide coding region
2460 - 3137	Yersenia pestis heavy chain Fab gene coding region
3167 - 3742	EMCV IRES
3743 - 3799	Bovine alpha-lactalbumin signal peptide coding region
3800 - 4441	Yersenia pestis light chain Fab gene coding region
4461 - 5052	WPRE sequence
5098 - 5691	Moloney murine leukemia virus 3' LTR

Figure 15
SEQ ID NO:12
IRES-Casein Signal Peptide Sequence

```
1     GGAATTCGCCCCTCTCCCTCCCCCCCCCCTAACGTTACTGGCCGAAGCCG
51    CTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTATTTTCCACCATAT
101   TGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGGCCCTGTCTTCTTG
151   ACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAGGAATGCAAGGTCT
201   GTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAA
251   CAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCCCCCACCTGGCGAC
301   AGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATACACCTGCAAAGGC
351   GGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCA
401   AATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAAGGATGCCCAGAAG
451   GTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGTGCACATGCTTTAC
501   ATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCCCCGAACCACGGGG
551   ACGTGGTTTTCCTTTGAAAAACACGATGATAATATGGCCTTGCTCATCCT
601   TACCTGTCTTGTGGCTGTTGCTCTTGCCGGCGCCATGGGATATCTAGATC
651   TCGAGCTCGCGAAAGCTT
```

1 - 583	IRES
584 - 628	Modified bovine alpha-S1 casein signal peptide coding region
629 - 668	Multiple cloning site

Figure 16a

SEQ ID NO: 13

LNBOTDC Vector

```
1     TTTGAAAGACCCCACCCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTT
51    TGCAAGGCATGGAAAAATACATAACTGAGAATAGAAAAGTTCAGATCAAG
101   GTCAGGAACAAAGAAACAGCTGAATACCAAACAGGATATCTGTGGTAAGC
151   GGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGAGACAGCTGAGTGATG
201   GGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCGGGGCCA
251   AGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAA
301   TCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAAATGACCCTGTACC
351   TTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTC
401   CGCTCTCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGCGCGCCA
451   GTCTTCCGATAGACTGCGTCGCCCGGGTACCCGTATTCCCAATAAAGCCT
501   CTTGCTGTTTGCATCCGAATCGTGGTCTCGCTGTTCCTTGGGAGGGTCTC
551   CTCTGAGTGATTGACTACCCACGACGGGGGTCTTTCATTTGGGGGCTCGT
601   CCGGGATTTGGAGACCCCTGCCCAGGGACCACCGACCCACCACCGGGAGG
651   TAAGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATG
701   TTTGATGTTATGCGCCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTAT
751   CTGGCGGACCCGTGGTGGAACTGACGAGTTCTGAACACCCGGCCGCAACC
801   CTGGGAGACGTCCCAGGGACTTTGGGGGCCGTTTTTGTGGCCCGACCTGA
851   GGAAGGGAGTCGATGTGGAATCCGACCCCGTCAGGATATGTGGTTCTGGT
901   AGGAGACGAGAACCTAAAACAGTTCCCGCCTCCGTCTGAATTTTTGCTTT
951   CGGTTTGGAACCGAAGCCGCGCGTCTTGTCTGCTGCAGCGCTGCAGCATC
1001  GTTCTGTGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATTA
1051  GGGCCAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAG
1101  ATGTCGAGCGGATCGCTCACAACCAGTCGGTAGATGTCAAGAAGAGACGT
1151  TGGGTTACCTTCTGCTCTGCAGAATGGCCAACCTTTAACGTCGGATGGCC
1201  GCGAGACGGCACCTTTAACCGAGACCTCATCACCCAGGTTAAGATCAAGG
1251  TCTTTTCACCTGGCCCGCATGGACACCCAGACCAGGTCCCCTACATCGTG
1301  ACCTGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGT
1351  ACACCCTAAGCCTCCGCCTCCTCTTCCTCCATCCGCCCCGTCTCTCCCCC
1401  TTGAACCTCCTCGTTCGACCCCGCCTCGATCCTCCCTTTATCCAGCCCTC
1451  ACTCCTTCTCTAGGCGCCGGAATTCCGATCTGATCAAGAGACAGGATGAG
1501  GATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCC
1551  GCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGG
1601  CTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTC
1651  TTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAGGACGAG
1701  GCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGT
1751  GCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAG
1801  TGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTA
1851  TCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTAC
1901  CTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTC
1951  GGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAG
2001  GGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCATGCCCGA
2051  CGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCA
2101  TGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGT
2151  GTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGA
2201  AGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCG
2251  CCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTC
2301  TTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAAC
2351  CTGCCATCACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGG
2401  CTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGG
2451  ATCTCATGCTGGAGTTCTTCGCCCACCCCGGGCTCGATCCCCTCGCGAGT
2501  TGGTTCAGCTGCTGCCTGAGGCTGGACGACCTCGCGGAGTTCTACCGGCA
2551  GTGCAAATCCGTCGGCATCCAGGAAACCAGCAGCGGCTATCCGCGCATCC
2601  ATGCCCCCGAACTGCAGGAGTGGGGAGGCACGATGGCCGCTTTGGTCGAG
2651  GCGGATCCGGCCATTAGCCATATTATTCATTGGTTATATAGCATAAATCA
2701  ATATTGGCTATTGGCCATTGCATACGTTGTATCCATATCATAATATGTAC
2751  ATTTATATTGGCTCATGTCCAACATTACCGCCATGTTGACATTGATTATT
```

Figure 16b

```
2801  GACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCAT
2851  ATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGA
2901  CCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCAT
2951  AGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTAC
3001  GGTAAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACG
3051  CCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCA
3101  GTACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAG
3151  TCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGT
3201  GGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGT
3251  CAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTC
3301  GTAACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCATGTACGGTGG
3351  GAGGTCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGCCTGGAG
3401  ACGCCATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCA
3451  GCCTCCGCGGCCCCAAGCTTCTCGACGGATCCCCGGGAATTCAGGCCATC
3501  GATCCCGCCGCCACCATGGAATGGAGCTGGGTCTTTCTCTTCTTCCTGTC
3551  AGTAACTACAGGTGTCCACTCCGACATCCAGATGACCCAGTCTCCAGCCT
3601  CCCTATCTGCATCTGTGGGAGAAACTGTCACTATCACATGTCGAGCAAGT
3651  GGGAATATTCACAATTATTTAGCATGGTATCAGCAGAAACAGGGAAAATC
3701  TCCTCAGCTCCTGGTCTATAATGCAAAAACCTTAGCAGATGGTGTGCCAT
3751  CAAGGTTCAGTGGCAGTGGATCAGGAACACAATATTCTCTCAAGATCAAC
3801  AGCCTGCAGCCTGAAGATTTTGGGAGTTATTACTGTCAACATTTTTGGAG
3851  TACTCCGTGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAACGGGCTG
3901  ATGCTGCACCAACTGTATCCATCTTCCCACCATCCAGTGAGCAGTTAACA
3951  TCTGGAGGTGCCTCAGTCGTGTGCTTCTTGAACAACTTCTACCCCAAAGA
4001  CATCAATGTCAAGTGGAAGATTGATGGCAGTGAACGACAAAATGGCGTCC
4051  TGAACAGTTGGACTGATCAGGACAGCAAAGACAGCACCTACAGCATGAGC
4101  AGCACCCTCACATTGACCAAGGACGAGTATGAACGACATAACAGCTATAC
4151  CTGTGAGGCCACTCACAAGACATCAACTTCACCCATTGTCAAGAGCTTCA
4201  ACAGGAATGAGTGTTGAAAGCATCGATTTCCCCTGAATTCGCCCCTCTCC
4251  CTCCCCCCCCCCTAACGTTACTGGCCGAAGCCGCTTGGAATAAGGCCGGT
4301  GTGCGTTTGTCTATATGTTATTTTCCACCATATTGCCGTCTTTTGGCAAT
4351  GTGAGGGCCCGGAAACCTGGCCCTGTCTTCTTGACGAGCATTCCTAGGGG
4401  TCTTTCCCCTCTCGCCAAAGGAATGCAAGGTCTGTTGAATGTCGTGAAGG
4451  AAGCAGTTCCTCTGGAAGCTTCTTGAAGACAAACAACGTCTGTAGCGACC
4501  CTTTGCAGGCAGCGGAACCCCCCACCTGGCGACAGGTGCCTCTGCGGCCA
4551  AAAGCCACGTGTATAAGATACACCTGCAAAGGCGGCACAACCCCAGTGCC
4601  ACGTTGTGAGTTGGATAGTTGTGGAAAGAGTCAAATGGCTCTCCTCAAGC
4651  GTATTCAACAAGGGGCTGAAGGATGCCCAGAAGGTACCCCATTGTATGGG
4701  ATCTGATCTGGGGCCTCGGTGCACATGCTTTACATGTGTTTAGTCGAGGT
4751  TAAAAAAACGTCTAGGCCCCCCGAACCACGGGGACGTGGTTTTCCTTTGA
4801  AAAACACGATGATAATATGGCCTCCTTTGTCTCTCTGCTCCTGGTAGGCA
4851  TCCTATTCCATGCCACCCAGGCCGAGGTTCAGCTTCAGCAGTCTGGGGCA
4901  GAGCTTGTGAAGCCAGGGGCCTCAGTCAAGTTGTCCTGCACAGCTTCTGG
4951  CTTCAACATTAAAGACACCTTTATGCACTGGGTGAAGCAGAGGCCTGAAC
5001  AGGGCCTGGAGTGGATTGGAAGGATTGATCCTGCGAATGGGAATACTGAA
5051  TATGACCCGAAGTTCCAGGGCAAGGCCACTATAACAGCAGACACATCCTC
5101  CAACACAGTCAACCTGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCG
5151  TCTATTACTGTGCTAGTGGAGGGGAACTGGGGTTTCCTTACTGGGGCCAA
5201  GGGACTCTGGTCACTGTCTCTGCAGCCAAAACGACACCCCCATCTGTCTA
5251  TCCACTGGCCCCTGGATCTGCTGCCCAAACTAACTCCATGGTGACCCTGG
5301  GATGCCTGGTCAAGGGCTATTTCCCTGAGCCAGTGACAGTGACCTGGAAC
5351  TCTGGATCCCTGTCCAGCGGTGTGCACACCTTCCCAGCTGTCCTGCAGTC
5401  TGACCTCTACACTCTGAGCAGCTCAGTGACTGTCCCCTCCAGCACCTGGC
5451  CCAGCGAGACCGTCACCTGCAACGTTGCCCACCCGGCCAGCAGCACCAAG
5501  GTGGACAAGAAAATTGTGCCCAGGGATTGTACTAGTGGAGGTGGAGGTAG
5551  CCACCATCACCATCACCATTAATCTAGAGTTAAGCGGCCGTCGAGATCTA
5601  GGCCTCCTAGGTCGACATCGATAAAATAAAAGATTTTATTTAGTCTCCAG
5651  AAAAAGGGGGGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCTAGCTTA
5701  AGTAACGCCATTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGAGA
5751  AGTTCAGATCAAGGTCAGGAACAGATGGAACAGCTGAATATGGGCCAAAC
5801  AGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGA
5851  TGGAACAGCTGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCT
```

Figure 16c

```
5901  GCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCT
5951  CAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGACCT
6001  GAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCT
6051  TCTGTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAACCC
6101  CTCACTCGGGGCGCCAGTCCTCCGATTGACTGAGTCGCCCGGGTACCCGT
6151  GTATCCAATAAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTT
6201  CCTTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTT
      TCATT
```

Moloney Murine Sarcoma Virus 5' LTR	1 - 589
Moloney Murine Leukemia Virus Extended Packaging Region	659 - 1468
Neomycin Resistance Gene	1512 - 2306
CMV Promoter	2656 - 3473
cc49 Signal Peptide Coding Region	3516 - 3572
Bot Fab 5 Light Chain	3573 - 4217
EMCV IRES (Clonetech)	4235 - 4816
Modified Bovine α-LA Signal Peptide Coding Region	4817 - 4873
Bot Fab 5 Heavy Chain	4874 - 5572
Moloney Murine Leukemia Virus 3' LTR	5662 - 6255

Figure 17a
SEQ ID NO: 34
LNBOTDC Vector

```
   1 GAATTAATTCATACCAGATCACCGAAAACTGTCCTCCAAATGTGTCCCCC
  51 TCACACTCCCAAATTCGCGGGCTTCTGCCTCTTAGACCACTCTACCCTAT
 101 TCCCCACACTCACCGGAGCCAAAGCCGCGGCCCTTCCGTTTCTTTGCTTT
 151 TGAAAGACCCCACCCGTAGGTGGCAAGCTAGCTTAAGTAACGCCACTTTG
 201 CAAGGCATGGAAAAATACATAACTGAGAATAGAAAAGTTCAGATCAAGGT
 251 CAGGAACAAAGAAACAGCTGAATACCAAACAGGATATCTGTGGTAAGCGG
 301 TTCCTGCCCCGGCTCAGGGCCAAGAACAGATGAGACAGCTGAGTGATGGG
 351 CCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCTCGGGGCCAAG
 401 AACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTTCTAGTGAATC
 451 ATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAAATGACCCTGTACCTT
 501 ATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGCGCGCTTCCG
 551 CTCTCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGGCGCGCCAGT
 601 CTTCCGATAGACTGCGTCGCCCGGGTACCCGTATTCCCAATAAAGCCTCT
 651 TGCTGTTTGCATCCGAATCGTGGTCTCGCTGTTCCTTGGGAGGGTCTCCT
 701 CTGAGTGATTGACTACCCACGACGGGGGTCTTTCATTTGGGGGCTCGTCC
 751 GGGATTTGGAGACCCCTGCCCAGGGACCACCGACCCACCACCGGGAGGTA
 801 AGCTGGCCAGCAACTTATCTGTGTCTGTCCGATTGTCTAGTGTCTATGTT
 851 TGATGTTATGCGCCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTATCT
 901 GGCGGACCCGTGGTGGAACTGACGAGTTCTGAACACCCGGCCGCAACCCT
 951 GGGAGACGTCCCAGGGACTTTGGGGGCCGTTTTTGTGGCCCGACCTGAGG
1001 AAGGGAGTCGATGTGGAATCCGACCCCGTCAGGATATGTGGTTCTGGTAG
1051 GAGACGAGAACCTAAAACAGTTCCCGCCTCCGTCTGAATTTTTGCTTTCG
1101 GTTTGGAACCGAAGCCGCGCGTCTTGTCTGCTGCAGCGCTGCAGCATCGT
1151 TCTGTGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATTAGG
1201 GCCAGACTGTTACCACTCCCTTAAGTTTGACCTTAGGTCACTGGAAAGAT
1251 GTCGAGCGGATCGCTCACAACCAGTCGGTAGATGTCAAGAAGAGACGTTG
1301 GGTTACCTTCTGCTCTGCAGAATGGCCAACCTTTAACGTCGGATGGCCGC
1351 GAGACGGCACCTTTAACCGAGACCTCATCACCCAGGTTAAGATCAAGGTC
1401 TTTTCACCTGGCCCGCATGGACACCCAGACCAGGTCCCCTACATCGTGAC
1451 CTGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTAC
1501 ACCCTAAGCCTCCGCCTCCTCTTCCTCCATCCGCCCCGTCTCTCCCCCTT
1551 GAACCTCCTCGTTCGACCCCGCCTCGATCCTCCCTTTATCCAGCCCTCAC
1601 TCCTTCTCTAGGCGCCGGAATTCCGATCTGATCAAGAGACAGGATGAGGG
1651 AGCTTGTATATCCATTTTCGGATCTGATCAGCACGTGTTGACAATTAATC
1701 ATCGGCATAGTATATCGGCATAGTATAATACGACAAGGTGAGGAACTAAA
1751 CCATGGCCAAGCCTTTGTCTCAAGAAGAATCCACCCTCATTGAAAGAGCA
1801 ACGGCTACAATCAACAGCATCCCCATCTCTGAAGACTACAGCGTCGCCAG
1851 CGCAGCTCTCTCTAGCGACGGCCGCATCTTCACTGGTGTCAATGTATATC
1901 ATTTTACTGGGGGACCTTGTGCAGAACTCGTGGTGCTGGGCACTGCTGCT
1951 GCTGCGGCAGCTGGCAACCTGACTTGTATCGTCGCGATCGGAAATGAGAA
2001 CAGGGGCATCTTGAGCCCCTGCGGACGGTGTCGACAGGTGCTTCTCGATC
2051 TGCATCCTGGGATCAAAGCGATAGTGAAGGACAGTGATGGACAGCCGACG
2101 GCAGTTGGGATTCGTGAATTGCTGCCCTCTGGTTATGTGTGGGAGGGCTA
2151 AGCACTTCGTGGCCGAGGAGCAGGACTGACACGTGCTACGAGATTTCGAT
2201 TCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGA
2251 CGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCG
2301 CCCACCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAAT
2351 AGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTG
2401 TGGTTTGTCCAAACTCATCAATGTATCTTATCATGTCTGTACGAGTTGGT
2451 TCAGCTGCTGCCTGAGGCTGGACGACCTCGCGGAGTTCTACCGGCAGTGC
2501 AAATCCGTCGGCATCCAGGAAACCAGCAGCGGCTATCCGCGCATCCATGC
2551 CCCCGAACTGCAGGAGTGGGGAGGCACGATGGCCGCTTTGGTCGAGGCGG
2601 ATCCGGCCATTAGCCATATTATTCATTGGTTATATAGCATAAATCAATAT
2651 TGGCTATTGGCCATTGCATACGTTGTATCCATATCATAATATGTACATTT
2701 ATATTGGCTCATGTCCAACATTACCGCCATGTTGACATTGATTATTGACT
2751 AGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATAT
2801 GGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGC
2851 CCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTA
```

Figure 17b

```
2901  ACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTA
2951  AACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCC
3001  CTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTAC
3051  ATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCAT
3101  CGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGAT
3151  AGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAAT
3201  GGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAA
3251  CAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCATGTACGGTGGGAGG
3301  TCTATATAAGCAGAGCTCGTTTAGTGAACCGTCAGATCGCCTGGAGACGC
3351  CATCCACGCTGTTTTGACCTCCATAGAAGACACCGGGACCGATCCAGCCT
3401  CCGCGGCCCCAAGCTTCTCGAGTTAACAGATCTAGGCTGGCACGACAGGT
3451  TTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAG
3501  CTCACTCATTAGGCACCCCAGGCTTTACACTTTATGCTTCCGGCTCGTAT
3551  GTTGTGTGGAATTGTGAGCGGATAACAATTTCACACAGGAAACAGCTATG
3601  ACCATGATTACGCCAAGCTTGGCTGCAGGTCGACGGATCCACTAGTAACG
3651  GCCGCCAGTGTGCTGGAATTCACCATGGGGCAACCCGGGAACGGCAGCGC
3701  CTTCTTGCTGGCACCCAATGGAAGCCATGCGCCGGACCACGACGTCACGC
3751  AGCAAAGGGACGAGGTGTGGGTGGTGGGCATGGGCATCGTCATGTCTCTC
3801  ATCGTCCTGGCCATCGTGTTTGGCAATGTGCTGGTCATCACAGCCATTGC
3851  CAAGTTCGAGCGTCTGCAGACGGTCACCAACTACTTCATCACAAGCTTGG
3901  CCTGTGCTGATCTGGTCATGGGGCTAGCAGTGGTGCCCTTTGGGGCCGCC
3951  CATATTCTCATGAAAATGTGGACTTTTGGCAACTTCTGGTGCGAGTTCTG
4001  GACTTCCATTGATGTGCTGTGCGTCACGGCATCGATTGAGACCCTGTGCG
4051  TGATCGCAGTCGACCGCTACTTTGCCATTACTAGTCCTTTCAAGTACCAG
4101  AGCCTGCTGACCAAGAATAAGGCCCGGGTGATCATTCTGATGGTGTGGAT
4151  TGTGTCAGGCCTTACCTCCTTCTTGCCCATTCAGATGCACTGGTACAGGG
4201  CCACCCACCAGGAAGCCATCAACTGCTATGCCAATGAGACCTGCTGTGAC
4251  TTCTTCACGAACCAAGCCTATGCCATTGCCTCTTCCATCGTGTCCTTCTA
4301  CGTTCCCCTGGTGATCATGGTCTTCGTCTACTCCAGGGTCTTTCAGGAGG
4351  CCAAAAGGCAGCTCCAGAAGATTGACAAATCTGAGGGCCGCTTCCATGTC
4401  CAGAACCTTAGCCAGGTGGAGCAGGATGGGCGGACGGGGCATGGACTCCG
4451  CAGATCTTCCAAGTTCTGCTTGAAGGAGCACAAAGCCCTCAAGACGTTAG
4501  GCATCATCATGGGCACTTTCACCCTCTGCTGGCTGCCCTTCTTCATCGTT
4551  AACATTGTGCATGTGATCCAGGATAACCTCATCCGTAAGGAAGTTTACAT
4601  CCTCCTAAATTGGATAGGCTATGTCAATTCTGGTTTCAATCCCCTTATCT
4651  ACTGCCGGAGCCCAGATTTCAGGATTGCCTTCCAGGAGCTTCTGTGCCTG
4701  CGCAGGTCTTCTTTGAAGGCCTATGGCAATGGCTACTCCAGCAACGGCAA
4751  CACAGGGGAGCAGAGTGGATATCACGTGGAACAGGAGAAAGAAAATAAAC
4801  TGCTGTGTGAAGACCTCCCAGGCACGGAAGACTTTGTGGGCCATCAAGGT
4851  ACTGTGCCTAGCGATAACATTGATTCACAAGGGAGGAATTGTAGTACAAA
4901  TGACTCACTGCTCTCGAGAATCGAGGGGCGGCACCACCATCATCACCACG
4951  TCGACCCCGGGGACTACAAGGATGACGATGACAAGTAAGCTTTATCCATC
5001  ACACTGGCGGCCGCTCGAGCATGCATCTAGCGGCCGCTCGAGGCCGGCAA
5051  GGCCGGATCCCCGGGAATTCGCCCCTCTCCCTCCCCCCCCCCTAACGTTA
5101  CTGGCCGAAGCCGCTTGGAATAAGGCCGGTGTGCGTTTGTCTATATGTTA
5151  TTTTCCACCATATTGCCGTCTTTTGGCAATGTGAGGGCCCGGAAACCTGG
5201  CCCTGTCTTCTTGACGAGCATTCCTAGGGGTCTTTCCCCTCTCGCCAAAG
5251  GAATGCAAGGTCTGTTGAATGTCGTGAAGGAAGCAGTTCCTCTGGAAGCT
5301  TCTTGAAGACAAACAACGTCTGTAGCGACCCTTTGCAGGCAGCGGAACCC
5351  CCCACCTGGCGACAGGTGCCTCTGCGGCCAAAAGCCACGTGTATAAGATA
5401  CACCTGCAAAGGCGGCACAACCCCAGTGCCACGTTGTGAGTTGGATAGTT
5451  GTGGAAAGAGTCAAATGGCTCTCCTCAAGCGTATTCAACAAGGGGCTGAA
5501  GGATGCCCAGAAGGTACCCCATTGTATGGGATCTGATCTGGGGCCTCGGT
5551  GCACATGCTTTACATGTGTTTAGTCGAGGTTAAAAAAACGTCTAGGCCCC
5601  CCGAACCACGGGGACGTGGTTTTCCTTTGAAAAACACGATGATAATATGG
5651  CCTCCTTTGTCTCTCTGCTCCTGGTAGGCATCCTATTCCATGCCACCCAG
5701  GCCGAGCTCACCCAGTCTCCAGACTCCCTGGCTGTGTCTCTGGGCGAGAG
5751  GGCCACCATCAACTGCAAGTCCAGCCAGAGTGTTTTGTACAGCTCCAACA
5801  ATAAGAACTATTTAGCTTGGTATCAGCAGAAACCAGGACAGCCTCCTAAG
5851  CTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATT
5901  CAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGC
5951  AGGCTGAAGATGTGGCAGTTTATTACTGTCAGCAATATTATAGTACTCAG
```

Figure 17c

6001 ACGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGAACTGTGGCTGCACC
6051 ATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACTG
6101 CCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTA
6151 CAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGT
6201 CACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGA
6251 CGCTGAGCAAAGCAGACTACGAGAAACACAAACTCTACGCCTGCGAAGTC
6301 ACCCATCAGGGCCTGAGATCGCCCGTCACAAAGAGCTTCAACAGGGGAG
6351 AGTGTTAGTTCTAGATAATTAATTAGGAGGAGATCTCGAGCTCGCGAAAG
6401 CTTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCG
6451 TTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCCTCCTA
6501 GGTCGACATCGATAAAATAAAAGATTTTATTTAGTCTCCAGAAAAAGGGG
6551 GGAATGAAAGACCCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCC
6601 ATTTTGCAAGGCATGGAAAAATACATAACTGAGAATAGAGAAGTTCAGAT
6651 CAAGGTCAGGAACAGATGGAACAGCTGAATATGGGCCAAACAGGATATCT
6701 GTGGTAAGCAGTTCCTGCCCCGGCTCAGGGCCAAGAACAGATGGAACAGC
6751 TGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGGCT
6801 CAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCAGCCCTCAGCAGTTT
6851 CTAGAGAACCATCAGATGTTTCCAGGGTGCCCCAAGGACCTGAAATGACC
6901 CTGTGCCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCTGTTCGC
6951 GCGCTTCTGCTCCCCGAGCTCAATAAAAGAGCCCACAACCCCTCACTCGG
7001 GGCGCCAGTCCTCCGATTGACTGAGTCGCCCGGGTACCCGTGTATCCAAT
7051 AAACCCTCTTGCAGTTGCATCCGACTTGTGGTCTCGCTGTTCCTTGGGAG
7101 GGTCTCCTCTGAGTGATTGACTACCCGTCAGCGGGGGTCTTTCATTTGGG
7151 GGCTCGTCCGGGATCGGGAGACCCCTGCCCAGGGACCACCGACCCACCAC
7201 CGGGAGGTAAGCTGGCTGCCTCGCGCGTTTCGGTGATGACGGTGAAAACC
7251 TCTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAAGCGGAT
7301 GCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTG
7351 TCGGGGCGCAGCCATGACCCAGTCACGTAGCGATAGCGGAGTGTATACTG
7401 GCTTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGC
7451 GGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGC
7501 TCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCG
7551 GCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAAT
7601 CAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCC
7651 AGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCC
7701 CCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACC
7751 CGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTG
7801 CGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCT
7851 CCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCA
7901 GTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCC
7951 GTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAA
8001 CCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGA
8051 TTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGG
8101 CCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCT
8151 GAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAC
8201 AAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACG
8251 CGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTC
8301 TGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGAT
8351 TATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTT
8401 AAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATG
8451 CTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTTCATCCA
8501 TAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTA
8551 CCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGC
8601 TCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAA
8651 GTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGG
8701 GAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGC
8751 CATTGCTGCAGGCATCGTGGTGTCACGCTCGTCGTTTGGTATGGCTTCAT
8801 TCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTG
8851 TGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAA
8901 GTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTC
8951 TTACTGTCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCA
9001 ACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCC
9051 GGCGTCAACACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGC

Figure 17d

```
9101  TCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCG
9151  CTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTC
9201  AGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGC
9251  AAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTC
9301  ATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCT
9351  CATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGG
9401  TTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATT
9451  ATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCG
   1.  TCTTCAAGAAT
```

Features:

```
149-737   Moloney murine sarcoma virus 5' LTR
807-1616  Extended Packaging Region
1680-1735  EM7 promoter (bacteriophage T7 promoter)
1754-2151  Blasticidin resistance gene coding sequence
2310-2440  SV40 poly A signal and site
2603-3420  CMV IE promoter
3675-4988 G-protein-coupled receptor (GPCR)
5071-5646  IRES
5647-5703  Bovine a-lactalbumin signal peptide
5704-6372 'humanized' antibody light chain
6553-7146  MoMuLV 3' LTR
7683Origin of replication
9302-8442  b-Lactmase coding sequence
```